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(54) Title: RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-x_L FUSION PROTEIN INHIBITS APOPTOSIS

(57) Abstract: Apoptosis-modifying fusion polypeptides, and the corresponding nucleic acid molecules, are disclosed. Pharmaceutical compositions comprising these polypeptides, and the use of these polypeptides to modify apoptosis are also provided.

RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-x_L FUSION PROTEIN INHIBITS APOPTOSIS

RELATED APPLICATIONS

This application claims priority based on U.S. provisional application number 60/149,220, filed August 16, 1999.

FIELD

This invention relates to modification of the apoptotic response of target cells, for instance target cells in a subject. More specifically, it relates to apoptosis-modifying fusion proteins with at least two domains, one of which targets the fusion protein to a target cell, and another of which modifies an apoptotic response of the target cell.

BACKGROUND

Tissue and cell homeostasis in multicellular organisms is largely influenced by apoptosis, the phenomenon of programmed cell death by which an intra- or extra-cellular trigger causes a cell to activate a biochemical "suicide" pathway. Morphological indicia of apoptosis include membrane blebbing, chromatin condensation and fragmentation, and formation of apoptotic bodies, all of which take place relatively early in the process of programmed cell death. Degradation of genomic DNA during apoptosis results in formation of characteristic, nucleosome sized DNA fragments; this degradation produces a diagnostic ~180bp laddering pattern when analyzed by gel electrophoresis. A later step in the apoptotic process is degradation of the plasma membrane, rendering apoptotic cells leaky to various dyes (*e.g.*, trypan blue and propidium iodide). Apoptotic cells are usually engulfed and destroyed early in the death process; thus, apoptosis tends not to be associated with inflammation caused by cytoplasm leakage, as is found in necrosis.

Various *in vivo* triggers can induce apoptosis; the paradigmatic trigger is a shortage of one or more necessary growth factors. Apoptosis plays a significant role in development of the neural system (reviewed in Cowan *et al.*, *Science* 225:1258-1265, 1984; Davies, *Development* 101:185-208, 1987; Oppenheim, *Annu. Rev. Neurosci.* 14:453-501, 1991) and lymphoid system (reviewed in Blackman *et al.*, *Science* 248:1335-1341, 1990; Rothenberg, *Adv. Immunol.* 51:85-214, 1992) of vertebrates. System development occurs through selective apoptotic extinction of certain cell populations.

In spite of much study, the molecular mechanisms of apoptosis are not fully elucidated. It does appear, however, that different apoptosis inducers may trigger different apoptotic pathways. For instance, certain pathways are transcription-dependent, in that apoptosis requires the synthesis of new proteins after stimulation by, for instance, withdrawal of growth factors. Staurosporine, a non-specific kinase inhibiter, in contrast, stimulates a transcription-independent pathway. Transcription dependent and independent pathways appear to share downstream components, including the ICE family of proteases (caspases). See Rubin, *British Med. Bulle.*, 53:617-631, 1997, for a review of apoptosis in

neurons; More general reviews include Ashkenazi and Dixit, *Science* 281:1305-1308; Thornberry and Lazebnik, *Science* 281:1312-1316; and Adams and Cory, *Science* 281:1322-1326.

Apoptosis is recognized as a gene-directed event, controlled by a complex set of interacting gene products that inhibit or enhance apoptosis (Williams and Smith, *Cell* 74:777-779, 1993; reviewed in White, *Genes Dev.* 10:1-15, 1996). Extensive effort is currently underway to identify and characterize the genes involved in this process. The first protein characterized as influencing apoptosis was Bcl-2 (Cleary *et al.*, *Cell* 47:19-28, 1986; Tsujimoto and Croce, *Proc. Natl. Acad. Sci. USA* 83:5214-5218, 1986). Since its discovery, several Bcl-2-related proteins (the Bcl-2 family of proteins) have been identified as being involved in regulation of apoptosis (White, *Genes Dev.* 10:1-15, 1996; Yang *et al.*, *Cell* 80:285-291, 1995). One such is Bcl-x, which is expressed in two different forms, long (Bcl-x_L) and short (Bcl-x_S) (Boise *et al.*, *Cell* 74:597-608, 1993).

Bcl-x_L and certain other members of the Bcl-2 family are, like Bcl-2 itself, powerful inhibitors of cell death (the "anti-death" Bcl-2 family members). Genetic overexpression of Bcl-2 has been shown to block apoptosis in the nervous system of transgenic mice (Chen *et al.*, *Nature* 385:434-439, 1997; Henkart, *Immunity* 4:195-201, 1996; Lippincott-Schwartz *et al.*, *Cell* 67:601-616, 1991; Hunziker *et al.*, *Cell* 67:617-627, 1991; Krajewski *et al.*, *Cancer Research* 53:4701-4714, 1993; Martinou *et al.*, *Neuron* 13:1017-1030, 1994).

Other members of the Bcl-2 protein family, including Bcl-x_S, Bad and Bax, are potent enhancers of apoptosis and therefore toxic to cells ("pro-death" Bcl-2 family members). Though the mechanism of apoptosis induction by these proteins remains unknown, it has been suggested that Bad binding to Bcl-x_L may promote cell death (Yang *et al.*, *Cell* 80:285-291, 1995; Zha *et al.*, *J Biol. Chem* 272:24101-24104, 1997) and that phosphorylation of Bad may prevent its binding to Bcl-x_L, thereby blocking cell death (Zha *et al.*, *J Biol. Chem.* 272:24101-24104, 1997; Zha *et al.*, *Cell* 87:619-628, 1996).

In addition to its involvement in neuronal and lymphoid system development and overall cell population homeostasis, apoptosis also plays a substantial role in cell death that occurs in conjunction with various disease and injury conditions. For instance, apoptosis is involved in the damage caused by neurodegenerative disorders, including Alzheimer's disease (Barinaga, *Science* 281:1303-1304), Huntington's disease, and spinal-muscular atrophy. There is also a substantial apoptotic component to the neuronal damage caused during stroke episodes (reviewed in Rubin, *British Med. Bulle.*, 53(3):617-631, 1997; and Barinaga, *Science* 281:1302-1303), and transient ischemic neuronal injury, as in spinal cord injury. It would be of great benefit to prevent undesired apoptosis in various disease and injury situations.

Treatment with standard apoptosis inhibitory molecules, for instance peptide-type caspase inhibitors (*e.g.*, DEVD-type), though useful for laboratory experiments where microinjection can be employed, has proven unsatisfactory for clinical work due to low membrane permeability of these inhibitors. Transfection of cells with various native proteins, including members of the Bcl-2 family of

regulatory proteins, has dual disadvantages. First, transfection is usually not cell-specific, and thus may disrupt apoptotic processes non-specifically in all cells. Second, transfection tends to provide long term alterations in the apoptotic process, in that once a transgene is integrated and functional in the genome of target cells, it may be difficult to turn off. Especially in instances of stroke episodes or transient ischemic neuronal injury, it would be more advantageous to be able to apply apoptosis regulation for short periods of time. Therefore, there is still a strong need to develop pharmaceutical agents that overcome these disadvantages.

Cancer and other hyper-proliferative cell conditions can be viewed as inappropriate escape from appropriate cell death. As such, it would be advantageous to be able to enhance apoptosis in certain of these cells to stop unregulated or undesired growth. Various attempts have been made to selectively eliminate cancerous cells through the use of targeted immunotoxins (genetic or biochemical fusions between a toxic molecule, for instance a bacterial toxin, and a targeting domain derived, typically from an antibody molecule).

One bacterial toxin that has been employed in attempts to kill cancerous cells is diphtheria toxin (DT). Diphtheria toxin has three structurally and functionally distinct domains: (1) a cell surface receptor binding domain (DTR), (2) a translocation domain (DTT) that allows passage of the active domain across the cell membrane, and (3) the A (enzymatically active) chain that, upon delivery to a cell, ADP-ribosylates elongation factor 2 and thereby inactivates translation. Altering the receptor specificity of the diphtheria toxin has been used to generate toxins that may selectively kill cancer cells *in vitro* (Thorpe *et al.*, *Nature* 271:752-755, 1978) and in man (Laske *et al.*, *Nature Medicine* 3:1362-1368, 1997). Promising though they might have seemed, these and similar hybrid immunotoxins have proven to be substantially less effective at targeted cell death than the toxins from which they were generated. This is perhaps due to difficulties in translocation of the fusion protein into the target cell (Columbatti *et al.*, *J. Biol. Chem.* 261:3030-3035, 1986). In addition, *in vivo* results have been particularly poor using such hybrid constructs (Fulton *et al.*, *Fed. Proc.* 461:1507, 1987).

It is to biological molecules that overcome deficiencies in the prior art that the present invention is directed.

SUMMARY OF THE DISCLOSURE

Disclosed herein are apoptosis-modifying fusion proteins constructed by fusing a protein, or an apoptosis-modifying fragment or variant thereof, from the Bcl-2 protein family with a cell-binding, targeting domain such as one derived from a bacterial toxin. Using this approach, apoptosis-modifying fusion proteins can be delivered effectively throughout the body and targeted to select tissues and cells. In certain embodiments, fusing various cell-binding domains to Bcl-2 family proteins (such as Bcl-x_L or Bad) allows targeting to specific subsets of cells *in vivo*, permitting treatment and/or prevention of the cell-death related consequences of various diseases and injuries. The delivery of other Bcl-2 homologues to the cell permits regulation of cell viability either positively (using anti-death Bcl-2 family members), or negatively (using pro-death members of the Bcl-2 family).

The apoptosis-modifying fusion proteins disclosed herein have specifiable cell-targeting and apoptosis-modifying activities. Thus, they may be used clinically to treat various disease and injury conditions, through inhibition or enhancement of an apoptotic cellular response. For instance, apoptosis-inhibiting fusion proteins are beneficial to minimize or prevent apoptotic damage that can be caused by neurodegenerative disorders (*e.g.*, Alzheimer's disease, Huntington's disease, spinal-muscular atrophy), stroke episodes, and transient ischemic neuronal injury (*e.g.*, spinal cord injury). The apoptosis-enhancing fusion proteins n can be used to inhibit cell growth, for instance uncontrolled cellular proliferation.

Accordingly, a first embodiment is a functional apoptosis-modifying fusion protein capable of binding a target cell, having a first domain capable of modifying apoptosis in the target cell, and a second domain capable of specifically targeting the fusion protein to the target cell. This fusion protein further integrates into or otherwise crosses a cellular membrane of the target cell upon binding to that cell.

Certain embodiments will also include a linker between these two domains. This linker will usually be at least 5 amino acids long, for example between 5 and 100 amino acids in length, and may for instance include the amino acid sequence shown in SEQ ID NO: 6. Appropriate linkers may be 6, 7, or 8 amino acids in length, and so forth, including linkers of about 10, 20, 30, 40 or 50 amino acids long.

The apoptosis modifying fusion proteins may also include a third domain from one of the two original proteins, or from a third protein. This third domain may improve the fusion protein's ability to be integrated into or otherwise cross a cellular membrane of the target cell. An example of such a third domain is the translocation region (domain or sub-domain) of diphtheria toxin.

Target cells for the fusion proteins disclosed herein include, but are not limited to, neurons, lymphocytes, stem cells, epithelial cells, cancer cells, neoplasm cells, and others, including other hyper-proliferative cells. The target cell chosen will depend on what disease or injury condition the fusion protein is intended to treat.

Receptor-binding domains may be derived from various cell-type specific binding proteins, including for instance bacterial toxins (*e.g.*, diphtheria toxin or anthrax toxin), growth factors (*e.g.*, epidermal growth factor), monoclonal antibodies, or single-chain antibodies derived from antibody genes. Further, variants or fragments of such proteins may also be used, where these fragments or variants maintain the ability to target the fusion protein to the appropriate target cell.

Further specific embodiments employ essentially the entire Bcl-x_L protein as the apoptosis-modifying domain of the fusion protein, or variants or fragments thereof that maintain the ability to inhibit apoptosis in a target cell to which the protein is exposed. Examples of such proteins are fusion proteins made of the Bcl-x_L protein, functionally linked to the diphtheria toxin receptor binding domain through a peptide linker of about six amino acids. One such protein is Bcl-x_L-DTR, which consists of Bcl-x_L and DTR, without the translocation domain of diphtheria toxin. The nucleotide sequence of this

fusion protein is shown in SEQ ID NO: 1, and the corresponding amino acid sequence in SEQ ID NOs: 1 and 2.

Another such example is LF_n-Bcl-x_L, which includes the amino terminal portion (residues 1-255) of mature anthrax lethal factor (LF), coupled to residues 1-209 of Bcl-x_L. The nucleotide sequence of this fusion protein is shown in SEQ ID NO: 7, and the corresponding amino acid sequence in SEQ ID NOs: 7 and 8.

Also encompassed are fusion proteins wherein the apoptosis-modifying domain is an apoptosis-enhancing domain. Such domains include the various pro-death members of the Bcl-2 family of proteins, for instance Bad, and variants or fragments thereof that enhance apoptosis in a target cell. A specific appropriate variant of the Bad protein has an amino acid other than serine at amino acid position 112 and/or position 136, to provide constitutively reduced phosphorylation.

Thus, one specific embodiment is a functional apoptosis-enhancing fusion protein capable of binding a target cell, comprising the Bad protein and the diphtheria toxin translocation and receptor binding domains, functionally linked to each other. The Bad protein of this embodiment can also contain a mutation(s) at position 112 and/or 136 to change the serine residue to some other amino acid, to reduce phosphorylation of the protein. One such protein is Bad-DTTR; the nucleotide sequence of this protein is shown in SEQ ID NO: 3, and the corresponding amino acid sequence in SEQ ID NOs: 3 and 4.

Also disclosed herein are nucleic acid molecules encoding apoptosis-modifying fusion proteins, for instance the nucleic acid sequences in SEQ ID NOs: 1, 3, and 7, and nucleic acid sequences having at least 90% sequence identity to these sequences, for instance those encoding for proteins containing one or more conservative amino acid substitutions. Other nucleic acid sequences may have 95% or 98% sequence identity with SEQ ID NO: 1, 3, or 7. Also encompassed are recombinant nucleic acid molecules in which such a nucleic acid sequence is operably linked to a promoter, vectors containing such a molecule, and transgenic cells comprising such a molecule.

Methods also are provided for producing functional recombinant apoptosis-modifying fusion proteins capable of binding to a target cell, integrating into or otherwise translocating across the cell membrane, and modifying an apoptotic response of the target cell. Such a protein can be produced in a prokaryotic or eukaryotic cell, for instance by transforming or transfecting such a cell with a recombinant nucleic acid molecule comprising a sequence which encodes a disclosed bispecific fusion protein. Appropriate eukaryotic cells include yeast, algae, plant or animal cells. Such transformed cells can then be cultured under conditions that cause production of the fusion protein, which is then recovered through protein purification means. The protein can include a molecular tag, such as a six histidine (hexa-his) tag, to facilitate its recovery.

Protein analogs, derivatives, or mimetics of the disclosed proteins, which retain the ability to target to appropriate target cells and modify apoptosis in those cells, are also encompassed in embodiments.

Compositions containing these apoptosis modifying fusion proteins, and analogs, derivatives, or mimetics of these proteins, are further aspects of this disclosure. Such compositions may further contain a pharmaceutically acceptable carrier, various other medical or therapeutic agents, and/or additional apoptosis modifying substances.

Methods for modifying apoptosis in a target cell are also encompassed, wherein a sufficient amount of a fusion protein of the current disclosure to modify apoptosis in the target cell is contacted with a target cell. Modification of apoptosis can be by either inhibition or enhancement of an apoptotic response of the target cell. The fusion protein can be administered to the target cell in the form of a pharmaceutical composition, and can further be administered with various medical or therapeutic agents, and/or additional apoptosis modifying substances. Such agents may include, for instance, chemotherapeutic, anti-inflammatory, anti-viral, and antibiotic agents.

Bcl-x_L-DTR, LF_n-Bcl-x_L, or related fusion proteins can be used to inhibit apoptosis in a target cell by contacting the target cell with an amount of this protein sufficient to inhibit apoptosis. Alternatively, Bad-DTTR or related fusion proteins can be used to enhance apoptosis in a target cell by contacting the target cell with an amount of this protein sufficient to enhance apoptosis.

A specific aspect disclosed herein is the method of reducing apoptosis in a subject after transient ischemic neuronal injury, for instance a spinal cord injury, comprising administering to the subject a therapeutically effective amount of an apoptosis-inhibiting protein according to this disclosure. Examples of such fusion proteins include Bcl-x_L-DTR and LF_n-Bcl-x_L. These proteins can be administered in the form of a pharmaceutical composition, and can be co-administered with various medical or therapeutic agents, and/or additional apoptosis modifying substances.

The foregoing and other features and advantages of the invention will become more apparent from the following detailed description of several embodiments, which proceeds with reference to the accompanying figures and tables.

BRIEF DESCRIPTION OF THE FIGURES

FIG 1 shows the construction, production and bioactivity of Bcl-x_L-DTR and Bcl-x_L transfected into HeLa cells. **FIG 1A** is a schematic representation of construction of Bcl-x_L-DTR. **FIG 1B** is a Western blot of the lysates of HeLa cells transiently transfected with Bcl-x_L (**lane b**) and Bcl-x_L-DTR (**lane c**). **Lane a** contains untransfected cells as a control. A small amount of endogeneous Bcl-x_L is present in lanes **a** and **c**. **FIG 1C** is a graph that shows transient transfection of Bcl-x_L (O) and Bcl-x_L-DTR (◇) genes into HeLa cells inhibits apoptotic cell death induced by the addition of STS. Apoptosis in control cells transfected with the vector (pcDNA3) vector is shown for comparison (□).

FIG 2 is a graph that shows the results of a diphtheria toxin receptor competitive binding assay. Cold competitor proteins [native DT (Δ), Bcl-x_L-DTR (▲), Bcl-x_L (O), and DTR (●)] were used to displace I^{125} labeled diphtheria toxin (DT) tracer, and the amount of bound, labeled tracer was measured. Native DT and the fusion protein Bcl-x_L-DTR compete for DT receptor binding in the nanomolar concentration range.

FIG 3 depicts the results of several experiments that demonstrate the apoptosis-inhibiting character of the fusion construct Bcl-x_L-DTR. Panel **A** is a graph of a time course of apoptosis induced by staurosporine (STS). Cells were treated with 0.1 μM STS (O), 0.1 μM STS plus 4.8 μM Bcl-x_L-DTR protein medium (Δ), or 20 μl of PBS (□). Results are presented as the average number of apoptotic cells per field (magnification 160 x). For each point, at least 5 fields were counted in each of at least 3 wells. **FIG 3B** is a SDS-PAGE gel that shows that Bcl-x_L-DTR prevents PARP cleavage. **Lane a** contains control HeLa cells not incubated with STS (uninduced cells); **Lane b**, HeLa cells treated with STS plus 1 μM Bcl-x_L-DTR protein; **Lane c**, HeLa cells treated with STS plus 1.48 μM Bcl-x_L-DTR protein; and **Lane d**, HeLa cells treated with STS and no fusion protein.

FIG 4 shows that Bcl-x_L-DTR inhibits of apoptosis induced by γ-radiation, but not that induced by α-Fas antibody. **FIG 4A** is a graph showing that the addition of Bcl-x_L-DTR prior to irradiation of Jurkat cells reduces apoptotic death in response to γ-radiation. Control cells were not irradiated and not treated with Bcl-x_L-DTR. **FIG 4B** is a graph that shows that, in Jurkat cells, Bcl-x_L-DTR had little inhibitory effect on apoptosis induced by anti-Fas antibody. Control cells were treated with PBS and no anti-Fas antibody.

FIG 5 shows that Bcl-x_L-DTR inhibits apoptosis induced by poliovirus.

FIG 6 is a graph showing the time course of viability of cells treated with Bad-DTTR.

FIG 7 shows the results of experiments that demonstrate that Bad-DTTR combined with STS triggers massive cell death. **FIG 7A** is a graph quantifying cell death after treatment of U251 MG cells with various combinations of STS and Bad-DTTR. Apoptosis is most enhanced when cells are treated with 0.1μM STS plus 0.65 μM Bad-DTTR, and cells begin to die about 12 hours after treatment. In the experiment depicted in **FIG 7B**, the use of 1 μM STS in combination with various concentrations of Bad-DTTR cause an earlier onset of apoptosis in U251 MG cells. Key: □ = PBS; ◇ = 0.1 μM STS; O = 0.65 μM Bad-DTTR; Δ = 0.065 μM Bad-DTTR; ⊞ = 0.1 μM STS + 0.65 μM Bad-DTTR; ⊖ = 0.1 μM STS + 0.065 μM Bad-DTTR.

FIG 8 is a schematic diagram of the chimera LF_n-Bcl-x_L. The fusion gene, LF_n-Bcl-x_L, was inserted into the vector, pET15b, yielding a histidine tag sequence at the N terminus of the LF_n-Bcl-x_L gene.

FIG 9 is a graph showing the time course of apoptosis induced by STS in J774 cells, with or without LF_n-Bcl-x_L protein. J774 cells at 3 x 10^4 / cm^2 were treated with 0.1 μM staurosporine alone, 0.1 μM staurosporine along with LF_n-Bcl-x_L (28 μg / ml) plus PA (33 μg / ml), or with PBS alone. The apoptotic and living cells were stained with Hoechst 33342 and counted at the indicated times, and the data were calculated as reported (Liu *et al.*, *Proc. Natl. Acad. Sci. USA* 96: 9563-9567, 1999).

FIG 10 is a bar graph showing the effect of LF_n-Bcl-x_L against J774 treated with STS. J774 cells at 10^4 / cm^2 were treated with PBS, 0.1 μM staurosporine alone, 0.1 μM staurosporine along with LF_n (28 μg/ml), 0.1 μM staurosporine along with Bcl-x_L (28 μg/ml), 0.1 μM staurosporine along with LF_n-Bcl-x_L (28 μg / ml), 0.1 μM staurosporine along with LF_n-Bcl-x_L (28 μg/ml) plus PA (33 μg/ml),

0.1 μM staurosporine along with PA (33 μg/ml) and 0.1 μM staurosporine along with LF_n (28 μg/ml) plus PA (33 μg/ml). The apoptotic and living cells were stained with Hoechst 33342 48 hours later and counted, and the data were calculated as for **FIG 9**.

FIG 11 is a bar graph showing the effect of LF_n-Bcl-x_L against Jurkat cells treated with STS. Jurkat cells at 10^5 / ml were treated with 0.1 μM staurosporine alone, 0.1 μM staurosporine along with LF_n-Bcl-x_L (28 μg / ml) plus PA (33 μg / ml) or with PBS. The apoptotic and living cells were stained with Hoechest 33342 21 hours later and counted, and the data were calculated as for FIG 9.

FIG 12 is a bar graph showing that the fusion protein LF_n-Bcl-x_L prevents apoptosis by in neonatal rat retinal ganglion cells 24 hours after optic nerve section. The apoptotic and living cells in retinal ganglion layers were counted 24 hours after optic nerve section immediately followed by the injection of PBS or the indicated protein(s). The percentage of apoptotic cells versus total retinal ganglion cells per retina is represented.

SEQUENCE LISTING

The nucleic and amino acid sequences listed in the accompanying sequence listing are shown using standard letter abbreviations for nucleotide bases, and three letter code for amino acids. Only one strand of each nucleic acid sequence is shown, but the complementary strand is understood as included by any reference to the displayed strand.

SEQ ID NO: 1 shows the DNA coding sequence and corresponding amino acid sequence of Bcl-x_L-DTR.

SEQ ID NO: 2 shows the amino acid sequence of Bcl-x_L-DTR.

SEQ ID NO: 3 shows the DNA coding sequence and corresponding amino acid sequence of Bad-DTTR.

SEQ ID NO: 4 shows the amino acid sequence of Bad-DTTR.

SEQ ID NO: 5 shows the nucleotide sequence of the linker used to link Bcl-x_L to DTR in the fusion construct Bcl-x_L-DTR.

SEQ ID NO: 6 shows the amino acid sequence of the linker used to link Bcl-x_L to DTR to form Bcl-x_L-DTR.

SEQ ID NO: 7 shows the DNA coding sequence and corresponding amino acid sequence of LF_n-Bcl-x_L.

SEQ ID NO: 8 shows the amino acid sequence of LF_n-Bcl-x_L.

DETAILED DESCRIPTION OF THE INVENTION

I. Abbreviations and Definitions

A. Abbreviations

DT: diphtheria toxin

DTR: diphtheria toxin receptor binding domain

DTT: diphtheria toxin translocation domain

DTTR: diphtheria toxin translocation and receptor binding domains

E. coli: *Escherichia coli*

EF: anthrax edema factor

LF: anthrax lethal factor

LF_n: first 255 residues of anthrax lethal factor

moi: multiplicity of infection

PA: anthrax protective antigen

PCR: polymerase chain reaction

RE: restriction endonuclease

SDS-PAGE: sodium dodecyl sulfate-polyacrylamide gel electrophoresis

STS: staurosporine

TdT: terminal deoxyribonucleotidyl transferase

TUNEL: TdT-dependent dUTP-biotin nick end labeling

B. Definitions

Unless otherwise noted, technical terms are used according to conventional usage. Definitions of common terms in molecular biology may be found in Lewin, Genes V published by Oxford University Press, 1994 (ISBN 0-19-854287-9); Kendrew *et al.*, (eds.), *The Encyclopedia of Molecular Biology*, published by Blackwell Science Ltd., 1994 (ISBN 0-632-02182-9); and Robert A. Meyers (ed.), *Molecular Biology and Biotechnology: a Comprehensive Desk Reference*, published by VCH Publishers, Inc., 1995 (ISBN 1-56081-569-8). The nomenclature for DNA bases and the three-letter code for amino acid residues, as set forth at 37 CFR § 1.822, are used herein.

In order to facilitate review of the various embodiments of the invention, the following definitions of terms are provided. These definitions are not intended to limit such terms to a scope narrower than would be known to a person of ordinary skill in the field.

Animal: Living multi-cellular vertebrate organisms, a category that includes, for example, mammals and birds. The term mammal includes both human and non-human mammals. Similarly, the term "subject" includes both human and veterinary subjects.

Apoptosis-modifying ability: A protein has apoptosis-modifying ability if it is capable of modifying apoptosis in a cell. This ability is usually measurable, either *in vivo* or *in vitro*, using any one of myriad apoptosis assays. The art is replete with methods for measuring apoptosis. Appropriate techniques include dye exclusion (*e.g.* Hoechst dye No. 33342), assaying for caspase activity, and TUNEL-staining. The specific ability of a fusion protein to modify the apoptotic response of a cell to various apoptosis-inducing stimuli can be determined by running standard apoptosis assays in the absence of or presence of various concentrations of the fusion proteins. The results of the assay are

then compared, and can be reported for instance by presenting the percentage of apoptosis that occurs in the presence of the fusion protein.

The invention also includes analogs, derivatives or mimetics of the disclosed fusion proteins, and which have apoptosis-modifying ability. Such molecules can be screened for apoptosis-modifying ability by assaying a protein similar to the disclosed fusion protein, in that it has one or more conservative amino acid substitutions or short in-frame deletions or insertions, or analogs, derivatives or mimetics thereof, and determining whether the similar protein, analog, derivative or mimetic provides modification of apoptosis in a desired target cell. The apoptosis-modifying ability and target cell binding affinity of these derivative compounds can be measured by any known means, including those discussed in this application.

Apoptosis-modifying fusion protein: Proteins that have at least two domains fused together, at least one domain comprising a cell binding region capable of targeting the fusion protein to a target cell (the targeting or cell-binding domain), and at least one domain capable of modifying apoptosis in the target cell (the apoptosis-modifying domain). The apoptosis-modifying fusion proteins of the current invention are further characterized by their ability to integrate into or otherwise cross a cellular membrane of the target cell when delivered extracellularly. An apoptosis-modifying fusion protein is considered functional if it targets to the correct target cell, and modifies an apoptotic response of that cell.

In general, the two domains of the disclosed fusions are genetically fused together, in that nucleic acid molecules that encode each protein domain are functionally linked together, for instance directly or through the use of a linker oligonucleotide, thereby producing a single fusion-encoding nucleic acid molecule. The translated product of such a fusion-encoding nucleic acid molecule is the apoptosis-modifying fusion protein.

Apoptosis-modifying fusion proteins can be labeled according to how they influence apoptosis in the target cell. For instance, an apoptosis-modifying fusion protein according to the current invention that inhibits apoptosis in the target cell can be referred to as an apoptosis-inhibiting fusion protein (*e.g.*, Bcl-x_L-DTR and LF_n-Bcl-x_L). Likewise, if the fusion protein enhances apoptosis in the target cell, it can be referred to as an apoptosis-enhancing fusion protein (*e.g.*, Bad-DTTR). Specific apoptosis-modifying fusion proteins are usually named for the proteins from which domains are taken to form the fusion, or from the domains actually used. For instance, "Bcl-x_L-DTR" (SEQ ID NOs: 1 and 2) consists of the entire Bcl-x_L protein fused in frame to the receptor-binding domain of diphtheria toxin (DTR) via a short linker.

A Bcl-2 protein: A Bcl-2 protein is a protein from the Bcl-2 family of proteins and includes those proteins related to Bcl-2 by sequence homology, which affect apoptosis. By way of example, the family includes Bcl-2, Bcl-x (both the long and short forms), Bax, and Bad. Additional members of the Bcl-2 family of proteins are known (Adams and Cory, *Science* 281:1322-1326, 1998).

Molecules that are derived from proteins of the Bcl-2 family include fragments of such proteins (*e.g.*, fragments of Bcl-x_L or Bad), generated either by chemical (*e.g.*, enzymatic) digestion or

genetic engineering means. Such fragments may comprise nearly all of the native protein, with one or a few amino acids being genetically or chemically removed from the amino or carboxy terminal end of the protein, or genetically removed from an internal region of the sequence.

Derived molecules, or **derived from**: The term "X-derived molecules" or "derived from X," where X is a protein also encompasses analogs (non-protein organic molecules), derivatives (chemically functionalized protein molecules obtained starting with the disclosed protein sequences) or mimetics (three-dimensionally similar chemicals) of the native protein structure, as well as proteins sequence variants or genetic alleles, that maintain biological functionality. Where the derived molecule is used as the targeting domain of an apoptosis-modifying fusion protein, the biological functionality maintained is the ability to target to fusion protein to the desired target cell. Likewise, where the derived molecule is used as the apoptosis-modifying domain of the fusion, the functionality maintained is the ability to affect apoptosis in the target cell. Each of these functionalities can be measured in various ways, including specific protein binding and apoptosis assays, respectively.

Injectable composition: A pharmaceutically acceptable fluid composition comprising at least one active ingredient, *e.g.*, an apoptosis-modifying fusion protein. The active ingredient is usually dissolved or suspended in a physiologically acceptable carrier, and the composition can additionally comprise minor amounts of one or more non-toxic auxiliary substances, such as emulsifying agents, preservatives, and pH buffering agents and the like. Such injectable compositions that are useful for use with the fusion proteins of this invention are conventional; appropriate formulations are well known in the art.

Isolated: An "isolated" biological component (such as a nucleic acid molecule, protein or organelle) has been substantially separated or purified away from other biological components in the cell of the organism in which the component naturally occurs, *i.e.*, other chromosomal and extra-chromosomal DNA and RNA, proteins and organelles. Nucleic acids and proteins that have been "isolated" include nucleic acids and proteins purified by standard purification methods. The term also embraces nucleic acids and proteins prepared by recombinant expression in a host cell as well as chemically synthesized nucleic acids.

Linker: A peptide, usually between two and 150 amino acid residues in length, which serves to join two protein domains in a multi-domain fusion protein. Peptide linkers are generally encoded for by a corresponding oligonucleotide linker. This can be genetically fused, in frame, between the nucleotides that encode the domains of a fusion protein.

Oligonucleotide: A linear polynucleotide sequence of between six and 300 nucleotide bases in length.

Operably linked: A first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked

DNA sequences are contiguous and, where necessary to join two protein-coding regions, in the same reading frame.

Parenteral: Administered outside of the intestine, *e.g.*, not via the alimentary tract. Generally, parenteral formulations are those that will be administered through any possible mode except ingestion. This term especially refers to injections, whether administered intravenously, intrathecally, intramuscularly, intraperitoneally, or subcutaneously, and various surface applications including intranasal, intradermal, and topical application, for instance.

Pharmaceutically acceptable carriers: The pharmaceutically acceptable carriers useful in this invention are conventional. Martin, *Remington's Pharmaceutical Sciences*, published by Mack Publishing Co., Easton, PA, 15th Edition, 1975, describes compositions and formulations suitable for pharmaceutical delivery of the fusion proteins herein disclosed.

In general, the nature of the carrier will depend on the particular mode of administration being employed. For instance, parenteral formulations usually comprise injectable fluids that include pharmaceutically and physiologically acceptable fluids such as water, physiological saline, balanced salt solutions, aqueous dextrose, glycerol or the like as a vehicle. For solid compositions (*e.g.*, powder, pill, tablet, or capsule forms), conventional non-toxic solid carriers can include, for example, pharmaceutical grades of mannitol, lactose, starch, or magnesium stearate. In addition to biologically-neutral carriers, pharmaceutical compositions to be administered can contain minor amounts of non-toxic auxiliary substances, such as wetting or emulsifying agents, preservatives, and pH buffering agents and the like, for example sodium acetate or sorbitan monolaurate.

Purified: The term purified does not require absolute purity; rather, it is intended as a relative term. Thus, for example, a purified fusion protein preparation is one in which the fusion protein is more enriched than the protein is in its generative environment, for instance within a cell or in a biochemical reaction chamber. Preferably, a preparation of fusion protein is purified such that the fusion protein represents at least 50% of the total protein content of the preparation. More purified preparations will have fusion protein that represents at least 60%, 70%, 80% or 90% of the total protein content.

Recombinant: A recombinant nucleic acid molecule is one that has a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two otherwise separated segments of sequence. This artificial combination can be accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, *e.g.*, by genetic engineering techniques.

Similarly, a recombinant protein is one encoded for by a recombinant nucleic acid molecule.

Sequence identity: The similarity between two nucleic acid sequences, or two amino acid sequences is expressed in terms of the similarity between the sequences, otherwise referred to as sequence identity. Sequence identity is frequently measured in terms of percentage identity (or similarity or homology); the higher the percentage, the more similar the two sequences are. Homologs of the apoptosis-modifying fusion protein will possess a relatively high degree of sequence identity when

aligned using standard methods. For instance, encoding sequences encompassed in the current invention include those that share about 90% sequence identity with SEQ ID NO: 1 and NO: 3.

Methods of alignment of sequences for comparison are well known in the art. Various programs and alignment algorithms are described in: Smith and Waterman, *Adv. Appl. Math.* 2:482, 1981; Needleman and Wunsch, *J. Mol. Biol.* 48:443, 1970; Pearson and Lipman, *PNAS.* USA 85:2444, 1988; Higgins and Sharp, *Gene*, 73:237-244, 1988; Higgins and Sharp, *CABIOS* 5:151-153, 1989; Corpet *et al.*, *Nuc. Acids Res.* 16:10881-90, 1988; Huang *et al.*, *Comp. Appls Biosci.* 8:155-65, 1992; and Pearson *et al.*, *Meth. Mol. Biol.* 24:307-31, 1994. Altschul *et al.*, *Nature Genet.* 6:119-29, 1994, presents a detailed consideration of sequence alignment methods and homology calculations.

The alignment tools ALIGN (Myers and Miller, *CABIOS* 4:11-17, 1989) or LFASTA (Pearson and Lipman, *PNAS.* USA 85:2444, 1988) may be used to perform sequence comparisons (Internet Program © 1996, W. R. Pearson and the University of Virginia, "fasta20u63" version 2.0u63, release date December 1996). ALIGN compares entire sequences against one another, while LFASTA compares regions of local similarity. These alignment tools and their respective tutorials are available on the Internet at the NCSA web-site.

For comparisons of amino acid sequences of greater than about 30 amino acids, the Blast 2 sequences function is employed using the default BLOSUM62 matrix set to default parameters, (gap existence cost of 11, and a per residue gap cost of 1). When aligning short peptides (fewer than around 30 amino acids), the alignment should be performed using the Blast 2 sequences function, employing the PAM30 matrix set to default parameters (open gap 9, extension gap 1 penalties). Proteins with even greater similarity to the reference sequences will show increasing percentage identities when assessed by this method, such as at least 90%, at least 92%, at least 94%, at least 95%, at least 97%, at least 98%, or at least 99% sequence identity.

An alternative indication that two nucleic acid molecules are closely related is that the two molecules hybridize to each other under stringent conditions. Stringent conditions are sequence-dependent and are different under different environmental parameters. Generally, stringent conditions are selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Conditions for nucleic acid hybridization and calculation of stringencies can be found in Sambrook *et al.*, In *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor, New York, 1989; and Tijssen, *Laboratory Techniques in Biochemistry and Molecular Biology* Part I, Ch. 2, Elsevier, New York, 1993. Nucleic acid molecules that hybridize to the disclosed apoptosis-modifying fusion protein sequences under stringent conditions will typically hybridize to a probe (based on the entire fusion protein encoding sequence, an entire domain, or other selected portions of the encoding sequence) under wash conditions of 0.2 x SSC, 0.1% SDS at 65°C.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences, due to the degeneracy of the genetic code. It is understood that changes in

nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that encode substantially the same protein.

Specific binding agent: An agent that binds substantially only to a defined target. Thus a Bcl-x_L-DTR-specific binding agent binds substantially only the Bcl-x_L-DTR protein in a specific preparation. As used herein, the term "Bcl-x_L-DTR-specific binding agent" includes Bcl-x_L-DTR antibodies and other agents that bind substantially only to a Bcl-x_L-DTR protein in that preparation.

Anti-Bcl-x_L-DTR antibodies may be produced using standard procedures described in a number of texts, including Harlow and Lane (*Using Antibodies, A Laboratory Manual*, CSHL, New York, 1999, ISBN 0-87969-544-7). The determination that a particular agent binds substantially only to Bcl-x_L-DTR protein may readily be made by using or adapting routine procedures. One suitable *in vitro* assay makes use of the Western blotting procedure (described in many standard texts, including Harlow and Lane, 1999). Western blotting may be used to determine that a given protein binding agent, such as an anti-Bcl-x_L-DTR monoclonal antibody, binds substantially only to the Bcl-x_L-DTR protein.

Alternately, because the disclosed apoptosis-modifying proteins are fusion proteins, they can be detected using antibodies to one or the protein domains used in their construction. For instance, fusions containing Bcl-x_L can be detected using the monoclonal antibody 2H12 (Hsu and Youle, *J. Biol. Chem.* 272:13829-13834, 1997; now available from Neo Markers, Union City, CA, clone #2H121-3) or other professionally available antibody preparations, for instance, polyclonal anti-Bcl-x_L/x_S #06-851 from Upstate Biotechnology, Lake Placid, NY; polyclonal rabbit anti-Bcl-x_L #65189E from PharMingen, San Diego, CA; and rabbit polyclonal (#B22630-050/B22630-150) or mouse monoclonal (B61220-050/B61220-150) anti-Bcl-x_L from Transduction Laboratories, Lexington, KY). Antibodies that recognize diphtheria toxin are, for instance, available from the Centers for Disease Control, Atlanta, GA.

Shorter fragments of antibodies can also serve as specific binding agents. For instance, FAbs, Fvs, and single-chain Fvs (SCFvs) that bind to Bcl-x_L-DTR would be Bcl-x_L-DTR-specific binding agents.

Target cell binding affinity: The physical interaction between a target cell and an apoptosis-modifying fusion protein as disclosed in this invention can be examined by various methods. Alternatively, the ability of fusion protein to compete for binding to its target cell with either native targeting domain or antibody that recognizes the targeting domain binding site on the target cell can be measured. This allows the calculation of relative binding affinities through standard techniques.

Therapeutically effective amount of an apoptosis-modifying fusion protein: A quantity of apoptosis-modifying fusion protein sufficient to achieve a desired effect in a subject being treated. For instance, this can be the amount necessary to measurably inhibit or enhance apoptosis in a target cell.

An effective amount of apoptosis-modifying fusion protein may be administered in a single dose, or in several doses, for example daily, during a course of treatment. However, the effective amount of fusion protein will be dependent on the fusion protein applied, the subject being treated, the severity and type of the affliction, and the manner of administration of the fusion protein. For example,

a therapeutically effective amount of fusion protein can vary from about 0.01 mg/kg body weight to about 1 g/kg body weight.

The fusion proteins disclosed in the present invention have equal application in medical and veterinary settings. Therefore, the general term "subject being treated" is understood to include all animals (*e.g.*, humans, apes, dogs, cats, horses, and cows), and particularly mammals, that are or may suffer from a chronic or acute condition or injury that causes apoptosis, or a lack thereof, susceptible to modification using molecules of the current invention.

Transformed: A transformed cell is a cell into which has been introduced a nucleic acid molecule by molecular biology techniques. As used herein, the term transformation encompasses all techniques by which a nucleic acid molecule might be introduced into such a cell, including transfection with viral vectors, transformation with plasmid vectors, and introduction of naked DNA by electroporation, lipofection, and particle gun acceleration.

Transgenic cell: A transgenic cell is one that has been transformed with a recombinant nucleic acid molecule.

Vector: A nucleic acid molecule as introduced into a host cell, thereby producing a transformed host cell. A vector may include nucleic acid sequences that permit it to replicate in a host cell, such as an origin of replication. A vector may also include one or more selectable marker genes and other genetic elements known in the art.

II. Construction, Expression, and Purification of Apoptosis-Modifying Fusion Proteins.

A. Selection of component domains.

This invention provides generally an apoptosis-modifying fusion protein that binds to a target cell, translocates across or otherwise integrates into the membrane(s) of the target cell, and modifies an apoptotic response of the target cell. As such, any target cell in which it is desirous to modify (either inhibit or enhance) apoptosis is an appropriate target for a bispecific fusion protein. The choice of appropriate protein binding domain for incorporation into the disclosed apoptosis-modifying fusion protein will be dictated by the target cell or cell population chosen. Examples of targeting domains include, for instance, nontoxic cell binding domains or components of bacterial toxins (such as diphtheria toxin or anthrax toxin), growth factors (such as epidermal growth factor), monoclonal antibodies, cytokines, and so forth, as well as targeting competent variants and fragments thereof.

The choice of appropriate Bcl-2 family member-derived apoptosis-modifying domain will depend on the manner in which the target cell's response to apoptosis is to be modified. Where apoptosis is to be inhibited by the resultant fusion protein, anti-death members of the Bcl-2 protein family are appropriate sources for apoptosis-modifying domains. One such fusion protein is Bcl-x_L-DTR, which employs the long form of Bcl-x, Bcl-x_L, as the apoptosis-modifying domain. Alternately, where enhancement of apoptosis is desired, pro-death members of the Bcl-2 family of proteins will be

appropriate. For instance, Bad-DTTR employs the pro-death protein Bad as its apoptosis-modifying domain.

Translocation of the apoptosis-modifying fusion protein into the target cell is important. A translocation domain may be included in the fusion protein as a separate, third domain. This could be supplied from a third protein, unrelated to the cell-binding and apoptosis-modifying domains, or be a translocation domain of one of these proteins (*e.g.*, the diphtheria toxin translocation (DTT) domain used in Bad-DTTR). The DTT domain contains several hydrophobic and amphipathic alpha helices and, after insertion into cell membranes, creates voltage dependent ion channels (Kagan *et al.*, *Proc Natl Acad Sci U S A* 78:4950-4954, 1981; Donovan *et al.*, *Proc Natl Acad Sci U S A* 78:172-176, 1981).

Alternately, the translocation function can be provided through the use of a cell-binding domain or apoptosis-modifying domain that confers the additional functionality of membrane translocation or integration. This is true in Bcl-x_L-DTR, wherein Bcl-x_L provides both the apoptosis-modifying ability and translocation into the cell.

B. Assembly

The construction of fusion proteins from domains of known proteins is well known. In general, a nucleic acid molecule that encodes the desired protein domains are joined using standard genetic engineering techniques to create a single, operably linked fusion oligonucleotide. Appropriate molecular biological techniques may be found in Sambrook *et al.*, In *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor, New York, 1989. Specific examples of genetically engineered multi-domain proteins, including those joined by various linkers, can be found in the following patent documents:

U.S. Patent No. 5,834,209 to Korsmeyer;

U.S. Patent No. 5,821,082 to Chinnadurai;

U.S. Patent No. 5,696,237 to FitzGerald *et al.*;

U.S. Patent No. 5,668,255 to Murphy;

U.S. Patent No. 5,587,455 to Berger *et al.*;

WO 98/17682 to Korsmeyer; and

WO 98/12328 to Horne *et al.*

It will usually be convenient to generate various control molecules for comparison to an apoptosis-modifying fusion protein, in order to measure the specificity of the apoptosis modification provided by each fusion protein. Appropriate control molecules may include one or more of the native proteins used in construction of the fusion, or fragments or mutants thereof.

C. Expression

One skilled in the art will understand that there are myriad ways to express a recombinant protein such that it can subsequently be purified. In general, an expression vector carrying the nucleic

acid sequence that encodes the desired protein will be transformed into a microorganism for expression. Such microorganisms can be prokaryotic (bacteria) or eukaryotic (*e.g.*, yeast). One appropriate species of bacteria is *Escherichia coli* (*E. coli*), which has been used extensively as a laboratory experimental expression system. A eukaryotic expression system will be preferred where the protein of interest requires eukaryote-specific post-translational modifications such as glycosylation. Also, protein can be expressed using a viral (*e.g.*, vaccinia) based expression system.

Protein can also be expressed in animal cell tissue culture, and such a system will be appropriate where animal-specific protein modifications are desirable or required in the recombinant protein.

The expression vector can include a sequence encoding a synthesis targeting peptide, positioned in such a way as to be fused to the coding sequence of the apoptosis-modifying fusion protein. This allows the apoptosis-modifying fusion protein to be targeted to specific sub-cellular or extra-cellular locations. Various appropriate prokaryotic and eukaryotic targeting peptides, and nucleic acid molecules encoding such, are well known to one of ordinary skill in the art. In a prokaryotic expression system, a signal sequence can be used to secrete the newly synthesized protein. In a eukaryotic expression system, the targeting peptide would specify targeting of the hybrid protein to one or more specific sub-cellular compartments, or to be secreted from the cell, depending on which peptide is chosen. Through the use of a eukaryotic secretion signal sequence, the apoptosis-modifying fusion protein can be expressed in a transgenic animal (for instance a cow, pig, or sheep) in such a manner that the protein is secreted into the milk of the animal.

Vectors suitable for stable transformation of culturable cells are also well known. Typically, such vectors include a multiple-cloning site suitable for inserting a cloned nucleic acid molecule, such that it will be under the transcriptional control of 5' and 3' regulatory sequences. In addition, transformation vectors include one or more selectable markers; for bacterial transformation this is often an antibiotic resistance gene. Such transformation vectors typically also contain a promoter regulatory region (*e.g.*, a regulatory region controlling inducible or constitutive expression), a transcription initiation start site, a ribosome binding site, an RNA processing signal, and a transcription termination site, each functionally arranged in relation to the multiple-cloning site. For production of large amounts of recombinant proteins, an inducible promoter is preferred. This permits selective production of the recombinant protein, and allows both higher levels of production than constitutive promoters, and enables the production of recombinant proteins that may be toxic to the expressing cell if expressed constitutively.

In addition to these general guidelines, protein expression/purification kits are produced commercially. See, for instance, the QIAexpress™ expression system from QIAGEN (Chatsworth, CA) and various expression systems provided by INVITROGEN (Carlsbad, CA). Depending on the details provided by the manufactures, such kits can be used for production and purification of the disclosed apoptosis-modifying fusion proteins.

D. Purification

One skilled in the art will understand that there are myriad ways to purify recombinant polypeptides, and such typical methods of protein purification may be used to purify the disclosed apoptosis-modifying fusion proteins. Such methods include, for instance, protein chromatographic methods including ion exchange, gel filtration, HPLC, monoclonal antibody affinity chromatography and isolation of insoluble protein inclusion bodies after over production. In addition, purification affinity-tags, for instance a six-histidine sequence, may be recombinantly fused to the protein and used to facilitate polypeptide purification. A specific proteolytic site, for instance a thrombin-specific digestion site, can be engineered into the protein between the tag and the fusion itself to facilitate removal of the tag after purification.

Commercially produced protein expression/purification kits provide tailored protocols for the purification of proteins made using each system. See, for instance, the QIAexpress™ expression system from QIAGEN (Chatsworth, CA) and various expression systems provided by INVITROGEN (Carlsbad, CA). Where a commercial kit is employed to produce a bispecific fusion protein, the manufacturer's purification protocol is a preferred protocol for purification of that protein. For instance, proteins expressed with an amino-terminal hexa-histidine tag can be purified by binding to nickel-nitrilotriacetic acid (Ni-NTA) metal affinity chromatography matrix (*The QIAexpressionist*, QIAGEN, 1997).

Alternately, the binding specificities of the cell-binding/targeting domain of the disclosed apoptosis-modifying protein may be exploited to facilitate specific purification of the proteins. A preferred method of performing such specific purification would be column chromatography using column resin to which the target cell surface receptor, or an appropriate epitope or fragment or domain of the target molecule, has been attached.

If the apoptosis-modifying fusion protein is produced in a secreted form, *e.g.* secreted into the milk of a transgenic animal, purification will be from the secreted fluid. Alternately, purification may be unnecessary if it is appropriate to apply the fusion protein directly to the subject in the secreted fluid (*e.g.* milk).

III. Variation of a Bispecific Fusion Protein

A. Sequence Variants

The binding and apoptosis-modifying characteristics of the apoptosis-modifying fusion proteins disclosed herein lies not in the precise amino acid sequence, but rather in the three-dimensional structure inherent in the amino acid sequences encoded by the DNA sequences. It is possible to recreate the functional characteristics of any of these proteins or protein domains of this invention by recreating the three-dimensional structure, without necessarily recreating the exact amino acid sequence. This can be achieved by designing a nucleic acid sequence that encodes for the three-dimensional structure, but which differs, for instance by reason of the redundancy of the genetic code.

Similarly, the DNA sequence may also be varied, while still producing a functional apoptosis-modifying fusion protein.

Variant apoptosis-modifying fusion proteins include proteins that differ in amino acid sequence from the disclosed sequence but that share structurally significant sequence homology with any of the provided proteins. Variation can occur in any single domain of the fusion protein (*e.g.*, the binding or apoptosis-modifying domain, or, where appropriate, the linker). Variation can also occur in more than one of such domains in any particular variant protein. Such variants may be produced by manipulating the nucleotide sequence of, for instance, a Bcl-x_L-encoding sequence, using standard procedures, such as site-directed mutagenesis or PCR. The simplest modifications involve the substitution of one or more amino acids for amino acids having similar biochemical properties. These so-called conservative substitutions are likely to have minimal impact on the activity of the resultant protein, especially when made outside of the binding site or active site of the respective domain. The regions or sub-domains of DTR that are essential to targeted cell binding are known in the art (see, Choe *et al.*, Nature 357:216-222, 1992; Parker and Pattus, TIBS 18:391-395, 1993). Regions or sub-domains of Bcl-2 proteins responsible for apoptosis modification are under intense study; much of this work is reviewed in Adams and Cory, *Science* 281:1322-1326.

Table 1 shows amino acids that may be substituted for an original amino acid in a protein, and which are regarded as conservative substitutions.

Table 1

Original Residue	Conservative Substitutions
Ala	ser
Arg	lys
Asn	gln; his
Asp	glu
Cys	ser
Gln	asn
Glu	asp
Gly	pro
His	asn; gln
Ile	leu; val
Leu	ile; val
Lys	arg; gln; glu
Met	leu; ile
Phe	met; leu; tyr
Ser	thr
Thr	ser
Trp	tyr
Tyr	trp; phe
Val	ile; leu

More substantial changes in protein structure may be obtained by selecting amino acid substitutions that are less conservative than those listed in Table 1. Such changes include changing residues that differ more significantly in their effect on maintaining polypeptide backbone structure

(*e.g.*, sheet or helical conformation) near the substitution, charge or hydrophobicity of the molecule at the target site, or bulk of a specific side chain. The following substitutions are generally expected to produce the greatest changes in protein properties: (a) a hydrophilic residue (*e.g.*, seryl or threonyl) is substituted for (or by) a hydrophobic residue (*e.g.*, leucyl, isoleucyl, phenylalanyl, valyl or alanyl); (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain (*e.g.*, lysyl, arginyl, or histadyl) is substituted for (or by) an electronegative residue (*e.g.*, glutamyl or aspartyl); or (d) a residue having a bulky side chain (*e.g.*, phenylalanine) is substituted for (or by) one lacking a side chain (*e.g.*, glycine).

Variant binding domain, apoptosis-modifying domain, or fusion protein-encoding sequences may be produced by standard DNA mutagenesis techniques, for example, M13 primer mutagenesis. Details of these techniques are provided in Sambrook *et al.*, In *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor, New York, 1989, Ch. 15. By the use of such techniques, variants may be created which differ in minor ways from the apoptosis-modifying fusion protein-encoding sequences disclosed. DNA molecules and nucleotide sequences which are derivatives of those specifically disclosed herein and that differ from those disclosed by the deletion, addition, or substitution of nucleotides while still encoding a protein that binds to a target cell, translocates or otherwise integrates into the target cell membrane(s), and thereby modifies an apoptotic response in the target cell, are comprehended by this invention. In their most simple form, such variants may differ from the disclosed sequences by alteration of the coding region to fit the codon usage bias of the particular organism into which the molecule is to be introduced.

Alternatively, the coding region may be altered by taking advantage of the degeneracy of the genetic code to alter the coding sequence such that, while the nucleotide sequence is substantially altered, it nevertheless encodes a protein having an amino acid sequence substantially similar to the disclosed fusion sequences. For example, the 57th amino acid residue of the Bcl-x_L-DTR protein is alanine. The nucleotide codon triplet GCC encodes this alanine residue. Because of the degeneracy of the genetic code, three other nucleotide codon triplets – (GCG, GCT and GCA) - also code for alanine. Thus, the nucleotide sequence of the disclosed Bcl-x_L-DTR encoding sequence could be changed at this position to any of these three alternative codons without affecting the amino acid composition or characteristics of the encoded protein. Based upon the degeneracy of the genetic code, variant DNA molecules may be derived from the cDNA and gene sequences disclosed herein using standard DNA mutagenesis techniques as described above, or by synthesis of DNA sequences. Thus, this invention also encompasses nucleic acid sequences which encode an apoptosis-modifying fusion protein, but which vary from the disclosed nucleic acid sequences by virtue of the degeneracy of the genetic code. Apoptosis assays, including those discussed herein, can be used to determine the ability of the resultant variant protein to modify apoptosis.

B. Peptide Modifications

The present invention includes biologically active molecules that mimic the action of the apoptosis-modifying fusion proteins of the present invention, and specifically modify apoptosis in a target cell. The proteins of the invention include synthetic versions of naturally-occurring proteins described herein, as well as analogues (non-peptide organic molecules), derivatives (chemically functionalized protein molecules obtained starting with the disclosed peptide sequences) and variants (homologs) of these proteins that specifically bind to a chosen target cell and modify apoptosis in that target cell. Each protein of the invention is comprised of a sequence of amino acids, which may be either L- and/or D- amino acids, naturally occurring and otherwise.

Proteins may be modified by a variety of chemical techniques to produce derivatives having essentially the same activity as the unmodified proteins, and optionally having other desirable properties. For example, carboxylic acid groups of the protein, whether carboxyl-terminal or side chain, may be provided in the form of a salt of a pharmaceutically-acceptable cation or esterified to form a C_1-C_{16} ester, or converted to an amide of formula NR_1R_2 wherein R_1 and R_2 are each independently H or C_1-C_{16} alkyl, or combined to form a heterocyclic ring, such as a 5- or 6- membered ring. Amino groups of the protein, whether amino-terminal or side chain, may be in the form of a pharmaceutically-acceptable acid addition salt, such as the HCl, HBr, acetic, benzoic, toluene sulfonic, maleic, tartaric and other organic salts, or may be modified to C_1-C_{16} alkyl or dialkyl amino or further converted to an amide.

Hydroxyl groups of the protein side chains may be converted to C_1-C_{16} alkoxy or to a C_1-C_{16} ester using well-recognized techniques. Phenyl and phenolic rings of the protein side chains may be substituted with one or more halogen atoms, such as fluorine, chlorine, bromine or iodine, or with C_1-C_{16} alkyl, C_1-C_{16} alkoxy, carboxylic acids and esters thereof, or amides of such carboxylic acids. Methylene groups of the protein side chains can be extended to homologous C_2-C_4 alkylenes. Thiols can be protected with any one of a number of well-recognized protecting groups, such as acetamide groups. Those skilled in the art will also recognize methods for introducing cyclic structures into the proteins of this invention to select and provide conformational constraints to the structure that result in enhanced stability.

Peptidomimetic and organomimetic embodiments are also within the scope of the present invention, whereby the three-dimensional arrangement of the chemical constituents of such peptido- and organomimetics mimic the three-dimensional arrangement of the protein backbone and component amino acid side chains in the apoptosis-modifying fusion protein, resulting in such peptido- and organomimetics of the proteins of this invention having measurable or enhanced neutralizing ability. For computer modeling applications, a pharmacophore is an idealized, three-dimensional definition of the structural requirements for biological activity. Peptido- and organomimetics can be designed to fit each pharmacophore with current computer modeling software (using computer assisted drug design or CADD). See Walters, Computer-Assisted Modeling of Drugs, *in* Klegerman & Groves (eds.),

Pharmaceutical Biotechnology, Interpharm Press: Buffalo Grove, IL, 165-174, 1993; and Munson (ed.) *Principles of Pharmacology*, Ch. 102, 1995, for descriptions of techniques used in CADD. Also included within the scope of the invention are mimetics prepared using such techniques that produce apoptosis-modifying fusion proteins.

IV. Activity of Fusion Proteins

Because the apoptosis modifying fusion proteins provided in this invention are at least bi-functional, having one domain required for cell targeting and another for modification of apoptosis in the target cell, there are at least two activities for each fusion protein. These include the affinity of the fusion protein for a specific target cell, class of target cells, tissue type, etc., (the binding ability), and the ability of the targeted fusion to effect apoptosis in the targeted cell (the apoptosis-modifying ability). Various techniques can be used to measure each of these activities.

A. Fusion protein affinity for target cells

Fusion protein affinity for the target cell, or to a specific cell surface protein, can be determined using various techniques known in the art. One common method is a competitive binding assay (Greenfield *et al.*, *Science* 238:536-539, 1987). In a competitive binding assay, radiolabeled receptor binding protein, or a derivative or fragment thereof, is exposed to the target native cell in the presence of one or varying concentrations of cold fusion protein and other competitive proteins being assayed. The amount of bound, labeled binding protein can be measured through standard techniques to determine the relative cell-binding affinity of the fusion.

B. Apoptosis inhibition or enhancement

Several *in vitro* systems are used to study the process of apoptosis. These include growth factor deprivation in culture, treatment of cells with staurosporine (a non-specific protein kinase inhibitor), application of γ-radiation, and infection by viruses. Apoptosis as stimulated by any signal can be examined or measured in a variety of ways. Detection of morphological indicia of apoptosis (*e.g.*, membrane blebbing, chromatin condensation and fragmentation, and formation of apoptotic bodies) can provide qualitative information. More quantitative techniques include TUNEL staining, measurement of DNA laddering, measurement of known caspase substrate degradation (*e.g.*, PARP; Taylor *et al.*, *J. Neurochem.* 68:1598-605, 1997) and counting dying cells, which have become susceptible to dye uptake. Many companies (*e.g.*, Trevigen, Gaithersburg MD; and R&D Systems, Minneapolis MN) also supply kits useful for the measurement of apoptosis by various methods; many of these kits can be used to measure the effect of disclosed apoptosis-modifying fusion proteins on apoptosis in a variety of cell types.

By way of example, the following techniques can be used to measure the modification of apoptosis caused in a target cell after it is contacted with an apoptosis-modifying fusion protein of the present invention.

TUNEL staining: Terminal end-labeling of broken DNA fragments with labeled nucleotides; the reaction is catalyzed by terminal nucleotide transferase (TdT). Various kits are available for measurement of TUNEL staining, including the TdT *in situ* TUNEL-based Kit (R&D Systems, Minneapolis, MN).

Measurement of Caspase Activity: Another common system for measuring the amount of apoptosis occurring in an *in vitro* cell system is to measure the poly-ADP ribose Polymerase (PARP) cleavage after treatment of the cells with various stimulators of apoptosis. PARP is a known substrate for a caspase (CPP-32) involved in the apoptotic kinase cascade. This technique can be carried out using essentially the following protocol. HeLa cells are plated in growth media (*e.g.*, EMEM containing 10% FBS at 2 x 10^5 cells/ml) and treated with one or more concentrations of an apoptosis-modifying fusion protein according to the current invention. The appropriate concentration for each fusion protein will depend on various factors, including the fusion protein in question, target cell, and apoptosis stimulator employed. Appropriate concentrations may include, for instance, about 0.5 μM to about 3 μM final. It may be beneficial to treat the target cells multiple times with the fusion protein, usually after a period of incubation ranging from one to several hours. For instance, cells can be exposed to the fusion protein a second time about fifteen hours after the original treatment. Usually the same concentration(s) of fusion protein is used in the second treatment.

Apoptosis is induced immediately the last treatment of the target cells with apoptosis modifying fusion protein. The method of application of the apoptosis stimulus, amount applied, appropriate incubation time with the inducer, etc., will be specific to the type of apoptosis induction used (*e.g.*, staurosporine, γ-radiation, virions, caspase inhibitor, etc.). Such details are in general well known to those of ordinary skill in the art. After an appropriate incubation period, cell lysates are prepared from the treated target cells, and aliquots loaded onto SDS-PAGE for analysis. The resultant gels can be examined using any of various well-known techniques, for instance by performing a Western analysis immunoblotted with anti-PARP polyclonal antibody (Boehringer Mannheim GmbH, Germany), developed with enhanced chemiluminescence.

Known inhibitors of apoptotic pathways, for instance caspase inhibitors, can be used to compare the effectiveness of apoptosis-modifying fusion proteins of this invention. Appropriate inhibitors include viral caspase inhibitors like crmA and baculovirus p35, and peptide-type caspase inhibitors including zVAD-fmk, YVAD- and DEVD-type inhibitors. See Rubin, *British Med. Bulle.*, 53:617-631, 1997.

V. Incorporation of Apoptosis-Modifying Fusion Proteins into Pharmaceutical Compositions

Pharmaceutical compositions that comprise at least one apoptosis modifying fusion protein as described herein as an active ingredient will normally be formulated with an appropriate solid or liquid carrier, depending upon the particular mode of administration chosen. The pharmaceutically acceptable carriers and excipients useful in this invention are conventional. For instance, parenteral

formulations usually comprise injectable fluids that are pharmaceutically and physiologically acceptable fluid vehicles such as water, physiological saline, other balanced salt solutions, aqueous dextrose, glycerol or the like. Excipients that can be included are, for instance, other proteins, such as human serum albumin or plasma preparations. If desired, the pharmaceutical composition to be administered may also contain minor amounts of non-toxic auxiliary substances, such as wetting or emulsifying agents, preservatives, and pH buffering agents and the like, for example sodium acetate or sorbitan monolaurate.

One or more other medicinal and pharmaceutical agents, for instance chemotherapeutic, anti-inflammatory, anti-viral or antibiotic agents, also may be included.

The dosage form of the pharmaceutical composition will be determined by the mode of administration chosen. For instance, in addition to injectable fluids, topical and oral formulations can be employed. Topical preparations can include eye drops, ointments, sprays and the like. Oral formulations may be liquid (*e.g.*, syrups, solutions or suspensions), or solid (*e.g.*, powders, pills, tablets, or capsules). For solid compositions, conventional non-toxic solid carriers can include pharmaceutical grades of mannitol, lactose, starch, or magnesium stearate. Actual methods of preparing such dosage forms are known, or will be apparent, to those skilled in the art.

The pharmaceutical compositions that comprise apoptosis modifying fusion protein will preferably be formulated in unit dosage form, suitable for individual administration of precise dosages. One possible unit dosage contains approximately 100 μg of protein. The amount of active compound administered will be dependent on the subject being treated, the severity of the affliction, and the manner of administration, and is best left to the judgment of the prescribing clinician. Within these bounds, the formulation to be administered will contain a quantity of the active component(s) in an amount effective to achieve the desired effect in the subject being treated. Ideally, a sufficient amount of the protein is administered to achieve tissue a concentration at the site of action that is at least as great as *in vitro* concentrations that have been shown to be effective.

VI. Clinical Use of Apoptosis-Modifying Fusion Proteins

The targeted apoptosis-regulating activity exhibited by the disclosed fusion proteins makes these fusions useful for treating neurodegenerative diseases, transient ischemic injuries, and unregulated cell growth (as may for instance be found in tumors and various cancers

The apoptosis-modifying fusion proteins of this invention may be administered to humans, or other animals on whose cells they are effective, in various manners such as topically, orally, intravenously, intramuscularly, intraperitoneally, intranasally, intradermally, intrathecally, and subcutaneously. Administration of apoptosis-modifying fusion protein composition is indicated for patients with a neurodegenerative disease, suffering from stroke episodes or transient ischemic injury, or experiencing uncontrolled or unwanted cell growth, such as malignancies or neoplasms. More generally, treatment is appropriate for any condition in which it would be beneficial to alter (either

inhibit or enhance) an apoptotic response of a subject's target cells. The particular mode of administration and the dosage regimen will be selected by the attending clinician, taking into account the particulars of the case (*e.g.*, the patient, the disease, and the disease-state involved). By way of example, when apoptosis is being generally inhibited over the short term, for instance after transient ischemic neuronal injury, it may be advantageous to administer relatively large doses of fusion protein repeatedly for a few days. In contrast, if apoptosis is being enhanced in specific cell types, for instance in hyper-proliferative cells, it may be of greater benefit to apply a relatively small dose of fusion protein repeatedly, *e.g.*, daily, weekly, or monthly, over a much longer period of treatment.

In addition to their individual use, apoptosis-modifying fusion proteins as disclosed in the current invention may be combined with various therapeutic agents. For instance, an apoptosis-enhancing fusion protein such as Bad-DTTR may be combined with or used in association with other chemotherapeutic or chemopreventive agents for providing therapy against neoplasms or other hyper-proliferative cellular growth conditions. Various such anti-cancer agents are well known to those of ordinary skill in the art. Apoptosis-modifying fusion proteins according to this invention also can be supplied in the form of kits; the construction of kits appropriate for therapeutically active proteins known.

EXAMPLE 1

Construction of functional apoptosis-modifying fusion proteins

A. Bcl-x_L-DTR

The human Bcl-x_L gene from codon 1 through 233 (provided by Dr. Craig Thompson) and the diphtheria toxin gene from codon 384 through 535 (receptor binding domain, DTR), containing mutations in codons 508 and 525, were amplified by PCR so that the DT mutation at codon 525 was mutated to the wild-type by the PCR primer. The two PCR products, Bcl-x_L1-233 and DT384-535 (DTR), were digested with NdeI / NotI and NotI / XhoI restriction enzymes, respectively. Bcl-x_L was fused to the 5′ end of the DTR gene with a linker (GCG TAT TCT GCG GCC GCG, SEQ ID NO: 5) to encode for Ala Tyr Ser Ala Ala Ala (SEQ ID NO: 6) between the two peptide domains. The two digested fragments were ligated into the prokaryotic expression vector pET16b (Novagen, Inc., Madison, WI) cut with NdeI and XhoI (FIG 1A). The codon 508 of DTR was mutated to the wild-type form (Phe → Ser) and the first three nucleotides (CAT) of NdeI were deleted by double-stranded, site-directed mutagenesis. FIG 1A shows a schematic representation of the resultant apoptosis-modifying fusion protein, Bcl-x_L-DTR.

As controls, human Bcl-x_L (codons 1-233) and DTR (codons 384-535 of DT) genes were separately subcloned into pET16b vectors through NdeI and XhoI sites. The histidine tag and Factor Xa digestion site sequences from the expression vector were upstream of Bcl-x_L, DTR and Bcl-x_L-DTR coding sequences. All three expression constructs were verified by sequencing.

For expression in eukaryotic cells, Bcl-x_L-DTR and Bcl-x_L gene constructs were inserted in the eukaryotic vector pcDNA3 (Invitrogen, Carlsbad, CA) and the constructs verified by sequencing.

B. Bad-DTTR

The full-length mouse Bad gene with two Ser → Ala mutations at codons 112 and 136 (Schendel *et al., Proc. Natl. Acad. Sci. USA* 94:5113-5118, 1997), and the diphtheria toxin gene from codons 194 through 535 (translocation and receptor-binding domains, DTTR, without the catalytic domain) were amplified by PCR. The two PCR products, Bad and DT194-535 (DTTR), were used as templates to directly fuse the Bad gene to the 5' end of DTTR gene by a second round of PCR. The Bad-DTTR gene fragment was digested with NdeI and XhoI and ligated into the prokaryotic expression vector pET16b (Novagen, Inc., Madison, WI) digested with NdeI and XhoI. The histidine tag and Factor Xa digestion site sequences from the expression vector were upstream of the Bad-DTTR coding sequence. The expression construct was verified by sequencing.

EXAMPLE 2

Expression and Purification of functional apoptosis-modifying fusion proteins

A. Prokaryotic Expression

To produce proteins for extracellular addition to cells, the Bcl-x_L gene, the DTR domain gene and the Bcl-x_L-DTR fusion gene were cloned into pET16b. *E. coli* BL21(DE3) strain was used to express Bcl-x_L-DTR, Bad-DTTR, Bcl-x_L and DTR, with addition of 1mM IPTG when the OD260 reached 0.5-0.7. After two hours incubation and lysis by French press the inclusion bodies were collected and dissolved in 6M guanidine-HCl.

B. Eukaryotic Expression

Transfection of HeLa cells with the fusion constructs was performed as reported previously (Wolter *et al., J Cell Biol* 139:1281-1292, 1997). HeLa cells were harvested and lysed in 1 ml buffer containing 100 μg / ml leupeptin 20 hours after transfection, centrifuged to remove cell debris, and 15 μl aliquots of the supernatant loaded onto 10-20% SDS-PAGE. The plasmid encoded proteins were visualized by immunoblotting with anti-Bcl-x_L monoclonal antibody (2H12, Trevigen, Gaithersburg, MD) and developed using enhanced chemiluminescence (Amersham Inc., Arlington Heights, IL). Results are shown in FIG 1B.

C. Purification

Histidine tag binding resin (Novagen, Inc., Madison, WI) was used to purify Bcl-x_L-DTR, Bad-DTTR, Bcl-x_L, and DTR. Proteins were refolded by dialysis against, or dilution into, 100 mM Tris-Acetate (pH 8.0) / 0.5 M arginine, concentrated with PEG15,000-20,000 and dialyzed against PBS. This yielded protein purified to greater than 90% homogeneity. The four proteins were subjected to 10-20% SDS-PAGE, visualized by immunoblotting with either anti-Bcl-x_L monoclonal (2H12) or horse anti-DT polyclonal antibodies (Centers for Disease Control, Atlanta, GA) and developed as above. They were of the expected molecular weight on SDS PAGE and of the expected immunoreactivity to antibodies against Bcl-x_L or DT on Western blots.

EXAMPLE 3

Assays for measuring fusion protein binding to, and translocation into, target cells

A. Competitive Binding Assay

Protein binding to the diphtheria toxin receptor was performed as previously reported (Greenfield *et al.*, *Science* 238:536-539, 1987) with the following modifications. DT was radiolabeled with I^{125} using iodobeads (Pierce Chem. Co., Rockford, IL) as described by the manufacturer. Cos-7 cells, grown to confluency in 12 well costar plates, were analyzed for receptor binding and competition by incubation for three hours on ice. Results are reported in FIG 2. Cold competitor proteins, native DT (Δ), Bcl-x_L-DTR (▲), Bcl-x_L (O), and DTR (●), were used to displace I^{125} labeled DT tracer.

Native DT and Bcl-x_L-DTR compete for DT receptor binding in the nanomolar concentration range. DT and the Bcl-x_L-DTR fusion protein competed for I^{125}-DT binding to its receptor to a similar extent although the affinity of the fusion was three times lower than that of native DT (FIG 2). Neither the Bcl-x_L domain alone nor the DTR domain alone was able to compete for DT receptor binding. The more complete protein (Bcl-x_L-DTR), where Bcl-x_L is substituted for the DT translocation domain, folded such that DT receptor binding activity was retained whereas the isolated binding domain (DTR) did not. Addition of the DT A chain domain to the N-terminus of Bcl-x_L-DTR further increased the affinity of the chimera to the DT receptor.

B. Assays for effective transport of the fusion protein into the target cell

Diphtheria toxin is endocytosed by cells and reaches low pH intracellular compartments. The low pH triggers a conformational change in the translocation domain, which allows this domain to insert into membranes and form channels. The toxicity of DT is blocked by lysosomotropic agents such as chloroquine, which increase the pH of intracellular compartments. Chloroquine at a concentration that blocks diphtheria toxin toxicity (10 μM) did not block the activity of Bcl-x_L-DTR to inhibit poliovirus-induced cell death. Thus, the mechanism of membrane interaction of Bcl-x_L-DTR differs to some extent from that of DT. However, brefeldin A, an inhibitor of vesicle traffic between the ER and the Golgi apparatus (Lippincott-Schwartz *et al.*, *Cell* 67:601-616, 1991; Hunziker *et al.*, *Cell* 67:617-627, 1991), does block the anti-apoptosis activity of Bcl-x_L-DTR (Table 3). These results indicate that Bcl-x_L-DTR must be endocytosed and suggest that Bcl-x_L-DTR must reach the Golgi apparatus or the ER to prevent cell death. The subcellular location from which native Bcl-2 family members regulate apoptosis is currently under scrutiny (Hunziker *et al.*, *Cell* 67:617-627, 1991). Several intracellular membrane locations, including the ER, appear able to mediate Bcl-2 family regulation of cell death (Krajewski *et al.*, *Cancer Res.* 53:4701-4714, 1993). Bcl-x_L-DTR may reach the ER to translocate into the cell cytosol or perhaps Bcl-x_L-DTR, when bound closely to a membrane, can insert into that membrane and inhibit apoptosis in the membrane-intercalated form.

EXAMPLE 4

Measurement of Bcl-x_L-DTR apoptosis-inhibiting activity

A. Apoptosis inhibition after transient cell transfection

To demonstrate that Bcl-x_L-DTR is effective at inhibiting apoptosis when expressed from within the target cell, this construct and the control construct containing Bcl-x_L were transiently transfected into HeLa cells. Assay of apoptosis inhibition after transient transfection was performed as reported previously (Wolter *et al., J. Cell Biol.* 139:1281-1292, 1997). The Bcl-x_L-DTR fusion gene blocked apoptosis after transient transfection into HeLa cells (FIG 1C) to an extent similar to that of the Bcl-x_L gene after C-terminal tail truncation (Wolter *et al., J Cell Biol* 139:1281-1292, 1997).

B. Inhibition of STS-induced apoptosis by extracellular treatment with Bcl-x_L-DTR

Hoechst dye no. 33342 staining: The effectiveness of extracellular delivery of Bcl-x_L or the Bcl-x_L-DTR fusion protein for inhibiting the rate of cell death by apoptosis was examined as follows. Cos-7 cells at 3 x 10^4 cells/cm^2 in 100 µl DMEM with 10% FBS were incubated with 0.1 µM STS (O), 0.1 µM STS plus 4.8 µM Bcl-x_L-DTR protein added to the medium (Δ) or 20 µl of PBS (□). Apoptotic cells were quantified by staining with Hoechst dye no. 33342. Results in FIG 3A are presented as the average number of cells per field (magnification 160 x). For each point, at least 5 fields were counted in each of at least 3 wells. Bcl-x_L-DTR dramatically decreased the rate of apoptosis in Cos-7 cells. Six different preparations of Bcl-x_L-DTR were found to have activity and the apoptosis prevention activity was stable for at least 5 months when Bcl-x_L-DTR was stored at 4 °C. Addition of Bcl-x_L-DTR minutes before the addition of STS blocked more than 70% of Cos-7 cell death after 6 hours and more than 50% of cell death after 12 hours of STS exposure (FIG 3A).

Jurkat, HeLa and U251 cells were also protected from STS-induced apoptosis by Bcl-x_L-DTR (Table 2). Bcl-x_L protein added to Cos-7 cells, however, did not alter the extent of cell death induced by STS. A nontoxic DT mutant able to bind the DT receptor, CRM197, also had no effect on apoptosis induced by STS. To further test the role of DT receptor binding in apoptosis inhibition, cells expressing DT receptors were compared with cells lacking DT receptors. Mouse and rat cells are thousands of times less sensitive to DT than human or monkey cell lines due to a lack of the DT receptor (Pappenheimer *The Harvey Lectures* 76:45-73, 1982). Comparing human, monkey, mouse and rat cell lines revealed that those cells lacking the DT receptor, WEHI-7.1 and 9L, were insensitive to apoptosis protection by Bcl-x_L-DTR (Table 2). The sensitivity of the six cell lines to DT toxicity, thought to reflect DT receptor levels, correlated with sensitivity to apoptosis prevention by Bcl-x_L-DTR (Table 2).

The magnitude of apoptosis inhibition by extracellular Bcl-x_L-DTR (FIG 3A, Table 2) was similar to that found by transfection of the fusion gene into cells (FIG 1C). Although fusion to the C-terminus of Bcl-x_L inhibited bioactivity relative to native Bcl-x_L after transfection (FIG 1C), a very substantial prevention of cell death was obtained at both the gene level and the protein level (FIG 3A).

Thus the delivery of Bcl-x_L-DTR is efficient and apoptosis can be prevented by delivery of Bcl-x_L from the outside of cells.

Measurement of caspase activity: To confirm the results of cell death measurements by Hoechst staining and trypan blue dye exclusion, we examined caspase-induced cleavage of poly-ADP ribose polymerase (PARP). HeLa cells were plated in EMEM containing 10% FBS at 2 x 10^5 cells/ml and treated with two different preparations of Bcl-x_L-DTR at 1.48 μM or 1 μM. Fifteen hours later, cells were treated again with Bcl-x_L-DTR at 1.48 μM or 1 μM. Immediately after the second treatment, 0.8 μM STS was added. Three hours later, cell lysates were made and aliquots were loaded onto SDS-PAGE, immunoblotted with anti-PARP polyclonal antibody (Boehringer Mannheim GmbH, Germany) and developed with enhanced chemiluminescence. **Lane a** contains control HeLa cells not incubated with STS (uninduced cells); **Lane b**, HeLa cells treated with STS plus 1 μM Bcl-x_L-DTR protein; **Lane c**, HeLa cells treated with STS plus 1.48 μM Bcl-x_L-DTR protein; and **Lane d**, HeLa cells treated with STS and no fusion protein. HeLa cells incubated with Bcl-x_L-DTR showed significantly less cleavage of PARP after apoptosis induction with STS (FIG 3B).

C. Inhibition of γ-radiation-induced apoptosis by extracellular treatment with Bcl-x_L-DTR

Radiation is a potent inducer of apoptosis in many hematopoetic cell types. The ability of Bcl-x_L-DTR to prevent radiation-induced apoptosis was examined in the human T cell line, Jurkat. When added to the media (serum-free RPMI-1640 medium with insulin and transferrin) of Jurkat cells plated at 10^5 cells/ml a few minutes prior to induction of apoptosis by 10 gray γ-radiation, Bcl-x_L-DTR (4.63 μM) blocked almost half of the ensuing cell death (FIG 4A). Apoptotic cells were counted using Hoechst dye no. 33342. Control cells were not irradiated and not treated with Bcl-x_L-DTR.

In a clonogenic assay measuring long term survival, Jurkat cells showed more than a 3-fold greater survival when Bcl-x_L-DTR was added to the media immediately prior to 5 gray γ-radiation.

D. Inhibition of anti-Fas-induced apoptosis by extracellular treatment with Bcl-x_L-DTR

Jurkat cells are also sensitive to apoptosis induced by antibody binding to the Fas/APO-1/CD95 receptor. The Fas pathway of apoptosis is one of the few pathways shown to be less sensitive or insensitive to apoptosis protection by Bcl-2 and Bcl-x_L (Boise & Thompson *Proc. Natl. Acad. Sci. USA* 94:3759-3764, 1997; Memon *et al., J. Immunol.* 155:4644-4652, 1995) and contrasts with radiation-induced apoptosis in this regard. Jurkat cells were plated at 10^5 cells/ml in serum-free RPMI-1640 medium with insulin and transferrin, and treated with 100 ng/ml anti-Fas antibody (CH11, Upstate Biotechnology, Lake Placid, NY) minutes after addition of Bcl-x_L-DTR to a concentration 4.68 μM. Control cells were treated with PBS and no anti-Fas antibody. Fas antigen-induced apoptosis (measured by counting dying cells using Hoechst dye no. 33342) showed very little inhibition by Bcl-x_L-DTR, although there was a statistically significant decrease in apoptosis between 2 and 4 hours in some experiments (FIG 4B). The degree of protection of different apoptosis pathways by extracellular Bcl-x_L-DTR corresponded with that seen by transfection with the Bcl-x_L gene.

E. Inhibition of poliovirus-induced apoptosis by extracellular treatment with Bcl-x_L-DTR

Viruses induce a powerful apoptosis response in certain cells and prevention of this apoptosis may have therapeutic utility (Hardwick, *Adv. Pharm.* 41:295-336, 1997). Poliovirus-induced apoptosis of HeLa cells was also examined for sensitivity to extracellular Bcl-x_L-DTR, a system where inhibition of cell death by transfection with the Bcl-x_L gene has been demonstrated (Castelli *et al.*, *J Exp. Med.* 186:967-972, 1997). Adding Bcl-x_L-DTR 30 minutes after infection of cells with low titers (MOI of 1 pfu / cell) of poliovirus (FIG 5) or with moderately high titers (MOI of 20 pfu / cell) of poliovirus prevented more than half of the cell death for up to 24 hours. Addition of extracellular Bcl-x_L or the DTR domain proteins alone had no affect on poliovirus-induced apoptosis.

F. Competition of apoptosis inhibition

Caspase inhibitors block many pathways of apoptosis and are being explored for pharmacologic potential to inhibit cell death (Chen *et al.*, *Nature* 385:434-439, 1997). zVAD-fmk and Boc-D-fmk are powerful, broad specificity caspase inhibitors that block many apoptosis pathways (Henkart, *Immunity* 4:195-201, 1996). Apoptosis inhibition activity of zVAD-fmk and Boc-D-fmk was compared with that of Bcl-x_L-DTR. HeLa cells were plated at a density of 1×10^5 cells/well in EMEM containing 10% FBS and antibiotics, infected with poliovirus at an MOI of 1 pfu/cell as reported previously (Castelli *et al.*, *J Exp Med* 186:967-972, 1997) and immediately treated with negative control peptide zFA-fmk at 20 μM, Bcl-x_L-DTR at 0.48 μM, or peptides zVAD-fmk or Boc-D-fmk at 20 μM. Cell viability was assessed by trypan blue dye exclusion 24 hours following addition of virus. zFA-fmk, zVAD-fmk and Boc-D-fmk were from Enzyme Systems Products, Dublin, CA.

Bcl-x_L-DTR at 0.48 μM blocked cell death to a greater extent than either zVAD-fmk or Boc-D-fmk at 20 μM (FIG 5). Bcl-x_L-DTR showed a strong inhibition of a potent and pathologically important apoptosis pathway. Interestingly, Bcl-x_L appears to act at an early step in the cell death pathway when intervention can permit long term viability of cells, whereas caspase inhibitors appear to work relatively more downstream in the apoptosis pathway (Chinnaiyan *et al.*, *J Biol Chem* 271:4573-4576, 1996; Xiang *et al.*, *Proc. Natl. Acad. Sci. USA* 93:14559-14563, 1996; Miller *et al.*, *J. Cell Biol* 139:205-217, 1997).

EXAMPLE 5

Measurement of Bad-DTTR apoptosis-enhancing activity

A. Stimulation of apoptosis by extracellular treatment with Bad-DTTR

To determine the effectiveness of the fusion protein Bad-DTTR at triggering apoptosis, cell survival after exposure to Bad-DTTR was examined. U251 MG cells at 3×10^4 cells/cm^2 in 100 μl DMEM with 10% FBS were incubated with 0.65 μM Bad-DTTR protein added to the medium or 20 μl of PBS. Total and apoptotic cells were quantified by staining with Hoechst dye no. 33342. Results

are presented in FIG 6 as the average number of cells per field (magnification 160 x). Bad-DTTR decreases cell viability 12 hours after treatment.

B. Enhancement of STS-triggered apoptosis by extracellular treatment with Bad-DTTR

To examine the ability of Bad-DTTR to enhance apoptosis triggered by STS, cell survival was determined after exposure to various concentrations of STS, in combination with various combinations of Bad-DTTR. U251 MG cells at 3 x 10^4 cells/cm^2 in 100 µl DMEM with 10% FBS were treated with PBS, 0.1µM STS, 0.65 µM Bad-DTTR, 0.065 µM Bad-DTTR, 0.1µM STS plus 0.65 µM Bad-DTTR and 0.1 µM STS plus 0.065 µM Bad-DTTR. Apoptotic death cells were quantified at different times by staining with Hoechst dye no. 33342. Results are presented as the average number of cells per field (magnification 160 x). Apoptosis is most enhanced when cells are treated with 0.1µM STS plus 0.65 µM Bad-DTTR, and cells begin to die about 12 hours after treatment.

U251 MG cells at 3 x 10^4 cells/cm^2 in 100 µl DMEM with 10% FBS were treated with PBS, 1µM STS, 0.65 µM Bad-DTTR, 0.065 µM Bad-DTTR, 1µM STS plus 0.65 µM Bad-DTTR and 1 µM STS plus 0.065 µM Bad-DTTR. Apoptotic cells were quantified and presented as above. The combination of 1 µM STS and Bad-DTTR at various concentrations causes an earlier onset of apoptosis in U251 MG cells.

EXAMPLE 6

LF_n-Bcl-x_L Inhibits Neuron, Macrophage, and Lymphocyte Apoptosis

Anthrax toxin includes three components: lethal factor (LF), edema factor (EF) and protective antigen (PA) (Leppla, *Anthrax toxin.* In *Handbook of Natural Toxins*, Moss *et al.*, Eds., Dekker, New York, Vol. 8, pp. 543-572, 1995). PA binds simultaneously to LF and to a cell surface receptor existing on the cells of almost all species including rodents (Leppla, 1995; Friedlander, *J. Biol. Chem.* 261:7123-7126, 1986), and transports LF into cells where LF causes toxic effects. PA alone, however, is not toxic. It has been found that the first 255 residues (LF_n) of LF, which constitute the PA-binding domain and are not toxic to cells, are sufficient for delivery of heterologous peptides to the cytosol. Cytotoxins have been fused to LF_n (Leppla, 1995; Arora *et al.*, *J Biol. Chem.* 269:26165-26171, 1994; Milne *et al.*, *Mol. Microbiol.* 15: 661-666, 1995). Administration of a fusion protein containing LF_n and the gp120 envelope glycoprotein of HIV-1 along with PA to antigen-presenting cells sensitized them to cytolysis by cytotoxic T-lymphocytes (CTL) specific to gp120 (Goletz *et al.*, *Proc Natl Acad Sci USA* 94:12059-12064, 1997). *In vivo*, LF_n-fused to CTL epitopes injected along with PA has been shown to stimulate a CTL response against the antigens in mice (Ballard *et al.*, *Proc. Natl. Acad. Sci. USA* 93: 12531-12534, 1996; Ballard *et al.*, *Infect. Immun.* 66:615-619, 1998; Ballard *et al.*, *Infect. Immun.* 66:4696-4699, 1998; Doling *et al.*, *Infect. Immun.* 67: 3290-3296, 1999).

To inhibit neuron apoptosis, another protein delivery system was engineered by fusing a nontoxic domain of anthrax toxin to Bcl-x_L, to create the LF_n-Bcl-x_L chimeric fusion protein. Macrophage and lymphocyte death in culture, and neuron death *in vivo* in a retinal ganglion cell model of apoptosis induced by axotomy, can be prevented by application of this fusion protein.

A. Construction of LF_n-Bcl-x_L in a prokaryotic expression plasmid

The coding sequence for lethal factor (LF) from codons 34 to 288 (LF_n) (Bragg *et al.*, *Gene* 81:45-54, 1989), which is the amino-terminal domain (residues 1-255) of mature LF (Leppla, 1995), was amplified using PCR with the template of pET15b/LF_n (Milne *et al.*, *Mol. Microbiol.* 15: 661-666, 1995). The gene of human Bcl-x_L from Codons 1 to 209 (Bcl-x_L(1-209)) (Boise *et al.*, *Cell* 74: 597-608, 1993) was amplified by PCR. Then the LF_n encoding sequence was fused to the 5′ end of Bcl-x_L(1-209) encoding sequence by a second round of PCR. A stop codon was introduced immediately after Codon 209 of Bcl-x_L. The fused DNA fragment, LF_n-Bcl-x_L, was cut with NdeI and Xho I, and inserted into prokaryotic expression vector pET15b cut with Nde I and Xho I (FIG 8). A histidine tag and thrombin cleavage site were linked to the N-terminal of LF_n-Bcl-x_L. Similarly, the Bcl-x_L gene from codons 1 to 209 was also genetically inserted into pET15b at the sites of Nde I and Xho I. All the constructs were verified by DNA sequencing.

B. Construction of eukaryotic expression plasmids, transfection, Western blotting and biologic activity assay

The sequences encoding LF_n-Bcl-x_L, Bcl-x_L from codons 1 to 209, and full-length Bcl-x_L, were separately engineered into eukaryotic expression vector pcDNA3.1+ and verified by DNA sequencing. Cos-7 cells were co-transfected with plasmid EGFP-C3 and one of the three plasmids as reported (Keith *et al.*, *J Cell Biol* 139: 1281-1292, 1997). The cells were treated with 0.1 μM staurosporine (STS) 12 hours later. The dead and living cells were counted with Hoechst 33342 at different times after STS treatment (Liu *et al.*, *Proc Natl Acad Sci USA* 96: 9563-9567, 1999; Keith *et al.*, *J Cell Biol* 139: 1281-1292, 1997). The cells were harvested and lysed 20 hours after transfection, and aliquots were loaded onto SDS/10-20% PAGE gels. The plasmid-encoded proteins were visualized by immunoblotting with anti-Bcl-x_L mAb (Trevigen, Gaithersburg, MD) and developed by using enhanced chemiluminescence (Amersham Pharmacia).

C. Protein expression, purification, SDS-PAGE and Western blotting

The proteins LF_n, LF_n-Bcl-x_L and Bcl-x_L from codons 1 to 209 were individually expressed in *E. coli* BL21(DE3) (Novagen, Inc.) and purified with a His•Tag binding purification kit (Novagen, Inc.). The transformed BL21(DE3) was cultured at 37°C in LB medium until the OD600 reached 0.5-0.8, and treated with 1mM IPTG, and then cultured for 3 more hours. The cells was pelleted, suspended in 1x His•Tag binding buffer with 1 mM phenylmethylsulfonyl fluoride (PMSF), 1 mM aprotinin and 1 mM leupeptin, and disrupted with French Press. The cytosol was separated from cell debris and undisrupted cells by centrifugation at 20,000 x g for 30 minutes and loaded on the His•Tag binding column. The eluted proteins were dialyzed against 1 x PBS and sterilized with 0.22-um filter.

Protective antigen (PA) was purified as reported (Milne *et al.*, *Mol. Microbiol.* 15: 661-666, 1995). The proteins were run on SDS-PAGE gels, and stained with Coomassie Blue or visualized by immunoblotting with anti-Bcl-x_L antibody, and developed as above.

D. J744 macrophage-like cell culture, treatment and apoptosis assay

J744 macrophage-like cells at 10^5/ ml were placed in 96-well plates (100 µl per well), and cultured overnight in RPMI 1640 with 10% FCS. The cells were treated with PBS, 0.1 µM staurosporine alone or 0.1 µM staurosporine along with the different combinations of the proteins LF_n-Bcl-x_L (28 µg/ml), PA (33 µg/ml), LF_n (28 µg/ml) and Bcl-x_L (28 µg/ml). The apoptotic and living cells were counted with Hoechst dye no. 33342 as reported (Liu *et al.*, *Proc Natl Acad Sci USA* 96: 9563-9567, 1999).

E. Optic nerve section and intra-ocular protein injection

The P0 pups of Fisher 344 rat strain were used for the present study. P0 is defined as the day of birth. The intracranial lesion of unilateral optic nerve was performed as reported (Rabachi *et al.*, *J Neurosci.*. 14: 5292-301, 1994). Briefly, a P0 pup was anesthetized by hypothermia. Under a dissecting microscope, an incision over the right eye was cut and a piece of bone flipped up. The right optic nerve was sectioned after suctioning the overlying cerebral cortex. The section site of optic nerve is about 3 mm away from the eyeball. A piece of gelfoam was put in the hole, and the flipped bone replaced, and the incision repaired with SUPERGLUE™. Immediately after the operation, seven, ten and four mice were respectively treated with administration of PBS, LF_n-Bcl-x_L (0.65 µg) plus PA (0.35 µg) and PA (0.35 µg) in a volume of 350 nanoliters (nl) per eye through ora serrata into the posterior chamber of the right eyes by using a micro-injector with a pulled micropipette. The pups were warmed up with a light lamp until the recovery, and then sent back to the mother. Four pups from the same litters, which were not operated and not treated, were used for normal control.

F. Histology

About 24 hours after sectioning of the optic nerve, the right eyes were removed under deep anesthesia with sodium pentobarbital, fixed in 4% paraformaldehyde for approximately 30 hours, embedded in paraffin and cut at 6 µm. The eyes taken from the normal pups in the same litters were processed in the same way to serve as controls. The sections were rehydrated, stained with 0.2% cresyl violet, dehydrated, and mounted with DPX mountant. The number of pyknotic cells and the number of living cells were counted by the use of 40 x objective in the entire retinal ganglion cell layer of three sections per retina. The pyknotic cells were identified as reported (Rabachi *et al.*, *J. Neurosci.* 14: 5292-301, 1994). The values were presented as the percentage of pyknotic cells versus total cells per retina (FIG 12).

G. Results

The PA protein from the Anthrax bacillus binds cell receptors and can mediate the delivery of the anthrax LF protein to the cell cytosol where LF effects toxicity to cells. The N-terminal domain of LF binds to PA. When exogeneous peptides are fused to the N-terminal domain of LF (LF_n), they can

be delivered to the cell cytosol by PA. Deletion of the C-terminal region of LF prevents toxicity to cells. To deliver Bcl-x_L to cells, the N-terminal 255 amino acids of LF were fused to Bcl-x_L without including the C-terminal 24 hydrophobic amino acids of Bcl-x_L, as shown schematically in FIG 8. The nucleotide and amino acid sequences of the fusion protein, LF_n-Bcl-x_L, are shown in SEQ ID NOs: 7 and 8. The fusion protein was expressed in *E. coli* and purified to near homogeneity.

The bioactivity of the LF_n-Bcl-x_L was explored in J774 cells in tissue culture. LF_n-Bcl-x_L, at 28 micrograms per ml plus PA at 33 micrograms per ml was added to the media of cells at the time of apoptosis induction with 0.1 μM staurosporine (STS). Cells treated with staurosporine alone died by apoptosis over the following 36 hours as shown in FIG 9. When the cells were treated with LF_n-Bcl-x_L plus PA, most of the cell death was inhibited.

Controls were performed to explore the requirements for apoptosis inhibition. FIG 10 shows data demonstrating that J774 cells treated with LF_n alone, Bcl-x_L alone, LF_n-Bcl-x_L without PA, and PA without LF_n-Bcl-x_L were not protected from apoptosis induced by staurosporine, whereas LF_n-Bcl-x_L plus PA prevented more than half of the cell death. Jurkat cells were also protected from apoptosis by LF_n-Bcl-x_L plus PA (FIG 11).

This new strategy to block cell death was explored in an *in vivo* model of neuron apoptosis. Retinal ganglion cells were axotomized and immediately afterwards a mixture containing 0.35 μg of PA and 0.65 μg of LF_n-Bcl-x_L was injected into the eye. Control mice were either not axotomized, axotomized and injected with PBS, or axotomized and injected with PA alone. Mice were sacrificed 24 hours later, and the eyes examined histologically. An increase in pyknotic cells, *i.e.*, apoptotic cells (Rabachi *et al.*, *J Neurosci.*. 14: 5292-301, 1994), occurs in the ganglion layer 24 hours after axotomy. However, when eyes are injected with LF_n-Bcl-x_L and PA, much of the cell death is inhibited. PA alone did not prevent cell death. To quantitate the extent of cell death, the number of living and pyknotic cells in three entire ganglion layers in one eye from each of 4-10 mice was counted. The quantified results are shown in FIG 12. LF_n-Bcl-x_L inhibited more than half of the cell death due to neuron axotomy *in vivo*.

In view of the many possible embodiments to which the principles of our invention may be applied, it should be recognized that the illustrated embodiments are only preferred examples of the invention, and should not be taken as limitations on its scope. Rather, the scope of the invention is defined by the following claims. We therefore claim as our invention all that comes within the scope and spirit of these claims.

Table 2

Inhibition of Apoptosis by Bcl-x_L-DTR

Cell line	Apoptosis inducer	Concentration of Bcl-x_L-DTR (μM)	Time of STS Treatment (Hrs)	Apoptosis Prevention (%*)	DT IO_{50} (M)
Cos-7 (monkey kidney)	0.1 μM STS	4.8	12	58.4	$10^{-12} - 10^{-11}$
U251 (human glioma)	0.1 μM STS	4.68	16	57.5	$10^{-12} - 10^{-11}$
HeLa (human cervical Ca)	0.2 μM STS	2.17	10	32.4	$10^{-12} - 10^{-11}$
Jurkat (human T leukemia)	0.1 μM STS	4.68	12	21.2	10^{-9}
9L (rat gliosarcoma)	0.1μM STS	4.68	12	-5.4	$> 10^{-7}$
WEH7.1 (mouse T lymphoma)	0.1μM STS	4.68	12	0.5	$> 10^{-7}$

*Apoptotic cells were counted with Hoechst dye no. 33342 and the percent prevention from apoptosis was calculated as 1 – (number of apoptotic cells with STS and Bcl-x_L-DTR – number of apoptotic cells without STS and Bcl-x_L-DTR) / (number of apoptotic cells with STS – number of apoptotic cells without STS and Bcl-x_L-DTR) except for the non-adherent Jurkat and WEHI7.1 cells which were counted by trypan blue dye exclusion and % apoptosis prevention calculated as (number of living cells with STS and Bcl-x_L-DTR – number of living cells with STS) / (number of living cells without STS and Bcl-x_L-DTR).

Table 3

Brefeldin A prevents Bcl-x_L-DTR blockade of apoptosis

	PBS	0.1 μM STS	0.1 μM STS+ 2.24 μM Bcl-x_L-DTR	Bcl-x_L-DTR
Cell death (%)	**1**	**24**	**11**	56% protection
	2 μM brefeldin A	0.1 μM STS+ 2 μM brefeldin A	0.1 μM STS+ 2μM brefeldin A + 2.24 μM Bcl-x_L-DTR	Bcl-x_L-DTR + brefeldin A
Cell death (%)	**2**	**35**	**32**	9% protection

Apoptotic cells were counted with Hoechst dye no. 33342 14 hours after addition of STS and / or brefeldin A minutes after Bcl-x_L-DTR was added to Cos-7 cells. The protection percentage was calculated as 1 – (number of apoptotic cells with STS and Bcl-x_L-DTR – number of apoptotic cells without STS and Bcl- x_L-DTR) / (number of apoptotic cells with STS – number of apoptotic cells without STS and Bcl-x_L-DTR).

We claim:

1. A functional apoptosis-modifying fusion protein capable of binding a target cell, comprising:

(a) a first domain capable of modifying apoptosis in the target cell; and

(b) a second domain capable of specifically targeting the fusion protein to the target cell, wherein the fusion protein integrates into or otherwise crosses a cellular membrane of the target cell upon binding.

2. The fusion protein of claim 1, wherein the first domain is capable of inducing or enhancing apoptosis.

3. The fusion protein of claim 1, wherein the first domain is capable of inhibiting or reducing apoptosis.

4. The functional purified apoptosis-modifying fusion protein of claim 1, comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence shown in SEQ ID NO: 2;

(b) the amino acid sequence shown in SEQ ID NO: 4;

(c) the amino acid sequence shown in SEQ ID NO: 8; and

(d) amino acid sequences that differ from those specified in (a), (b), or (c) by one or more conservative amino acid substitutions, but which retain targeting and apoptosis-modifying abilities.

5. An isolated nucleic acid molecule encoding a protein according to claim 4.

6. The isolated nucleic acid molecule of claim 5 wherein the molecule comprises a sequence selected from the group consisting of:

(a) SEQ ID NO: 1;

(b) SEQ ID NO: 3;

(c) SEQ ID NO: 7; and

(d) nucleic acid sequences having at least 90% sequence identity to the sequences specified in (a), (b), or (c).

7. A recombinant nucleic acid molecule comprising a promoter sequence operably linked to a nucleic acid sequence according to claim 5.

8. A transgenic cell comprising a recombinant nucleic acid molecule according to claim 7.

9. The transgenic cell of claim 8, wherein the cell is a bacteria, a yeast, an algae, a plant; or an animal cell.

10. The functional apoptosis-modifying fusion protein of claim 1, further comprising:

(c) a linker connecting the first domain to the second domain.

11. The protein of claim 1, wherein the first domain is a Bcl-2 family protein, or a variant or fragment thereof that retains an apoptosis-modifying property.

12. The protein of claim 11, wherein the first domain is pro-apoptotic.

13. The protein of claim 11, wherein the first domain is anti-apoptotic.

14. The protein of claim 11, wherein the first domain is Bcl-x_L, or a variant or fragment thereof that inhibits apoptosis in the target cell to which the protein is exposed.

15. The protein of claim 14, wherein the first domain consists essentially of Bcl-x_L.

16. The protein of claim 11, wherein the first domain is Bad, or a variant or fragment thereof that enhances apoptosis in the target cell to which the protein is exposed.

17. The protein of claim 16, wherein the first domain is a variant of Bad having an amino acid other than serine at amino acid position 112 and/or position 136.

18. The protein of claim 16, wherein the first domain consists essentially of Bad.

19. The protein of claim 14, wherein the target cell is a neuron, a lymphocyte, a macrophage, an epithelial cell, or a stem cell.

20. The protein of claim 17, wherein the target cell is a tumor cell, a cancer cell, a neoplasm cell, a hyper-proliferative cell, or an adipocyte.

21. The protein of claim 1, wherein the second domain comprises a receptor-binding domain derived from a bacterial toxin, a monoclonal antibody, a growth factor, or a cytokine.

22. The protein of claim 21, wherein the second binding domain comprises a receptor-binding domain derived from diphtheria toxin or anthrax toxin.

23. The protein of claim 21, wherein the second binding domain comprises a receptor-binding domain derived from epidermal growth factor

24. The protein of claim 21, wherein the receptor-binding domain comprises diphtheria toxin receptor binding domain, or a variant or fragment thereof that targets the fusion protein to the target cell to which the protein is exposed.

25. The protein of claim 21, wherein the second domain further comprises a translocation domain of diphtheria toxin.

26. An isolated nucleic acid molecule encoding a fusion protein according to claim 1.

27. The protein of claim 10, wherein the linker is 5-100 amino acid residues in length.

28. The protein of claim 10, wherein the linker comprises the amino acid sequence shown in SEQ ID NO: 6.

29. The protein of claim 22, wherein the linker consists essentially of the amino acid sequence shown in SEQ ID NO: 6.

30. The functional apoptosis-modifying fusion protein of claim 1, comprising:

(a) Bcl-x_L;

(b) a bacterial toxin receptor binding domain; and

(c) a peptide linker of about 6 amino acids in length, functionally linking (a) to (b).

31. The fusion protein of claim 30, wherein (b) is a diphtheria toxin or anthrax toxin receptor binding domain.

32. The fusion protein of claim 30, which does not include a functional diphtheria toxin translocation domain.

33. The fusion of claim 31, wherein (b) comprises LF_n.

34. The fusion protein of claim 32, consisting essentially of:

(a) Bcl-x_L;

(b) a diphtheria toxin receptor binding domain; and

(c) a peptide linker of about 6 amino acids in length, functionally linking (a) to (b).

35. The protein of claim 30, wherein the linker has an amino acid sequence shown in SEQ ID NO: 6.

36. An isolated nucleic acid molecule encoding a protein according to claim 30.

37. The nucleic acid molecule of claim 36, wherein the nucleic acid sequence is represented by SEQ ID NO: 1.

38. The functional apoptosis-modifying fusion protein of claim 1, comprising:

(a) Bad;

(b) a diphtheria toxin translocation domain; and

(c) a bacterial toxin receptor binding domain,

wherein (a), (b), and (c) are functionally linked.

39. The fusion protein of claim 38, wherein (c) is a diphtheria toxin or anthrax toxin receptor binding domain.

40. An isolated nucleic acid molecule encoding a protein according to claim 38.

41. The nucleic acid molecule of claim 40, wherein the nucleic acid sequence is shown in SEQ ID NO: 3.

42. A method for producing in a cell a functional apoptosis-modifying fusion protein capable of binding a target cell, comprising the steps of:

(a) transfecting a cell with an isolated recombinant nucleic acid molecule of claim 25 to produce a transgenic cell;

(b) culturing the transgenic cell under conditions that cause production of the protein; and

(c) recovering the protein produced by the transgenic cell.

43. The method of claim 42, wherein the cell is a eukaryotic cell.

44. The method of claim 43, wherein the eukaryotic cell is a mammalian cell.

45. The method of claim 42, wherein recovering the protein comprises:

a) identifying the protein by the presence of a molecular tag; and

b) separating the protein having the molecular tag so identified from molecules without the tag, so as to recover the protein produced by the cultured transgenic cell.

46. A composition comprising the protein according to claim 1, or an analog or mimetic thereof.

47. A pharmaceutical composition comprising the composition according to claim 46, and a pharmaceutically acceptable carrier.

48. A combined pharmaceutical composition comprising a fusion protein according to claim 33, and a sufficient amount PA to enable measurable transport of the fusion protein into a target cell.

49. A method for modifying apoptosis in a target cell, comprising the step of:

contacting the target cell with an amount of the protein of claim 1 sufficient to modify apoptosis in the target cell.

50. The method of claim 49, wherein the protein is administered in the form of a pharmaceutical composition.

51. The method of claim 49, further comprising the step of co-administering an agent selected from the group consisting of a chemotherapeutic agent, an anti-inflammatory agent, an anti-viral agent, and an antibiotic agent.

52. The method of claim 49, wherein apoptosis in the target cell is inhibited.

53. The method of claim 49, wherein apoptosis in the target cell is enhanced.

54. A method for inhibiting apoptosis in a target cell, comprising the step of:

contacting the target cell with an amount of the protein of claim 14, sufficient to inhibit apoptosis.

55. A method for enhancing apoptosis in a target cell, comprising the step of:

contacting the target cell with an amount of the protein of claim 17, sufficient to enhance apoptosis.

56. A method of reducing apoptosis in a subject after transient ischemic neuronal injury, comprising administering to the subject a therapeutically effective amount of a protein of claim 14.

57. The method of claim 56, wherein the transient ischemic neuronal injury is a spinal cord injury.

58. The method of claim 56, wherein the protein is administered in the form of a pharmaceutical composition.

59. The method of claim 56, further comprising the step of co-administering an agent selected from the group consisting of a chemotherapeutic agent, an anti-inflammatory agent, an anti-viral agent, and an antibiotic agent.

60. A protein analog, derivative, or mimetic of the protein of claim 1.

61. The protein of any one of claims 1-4 for use in modifying apoptosis in a target cell.

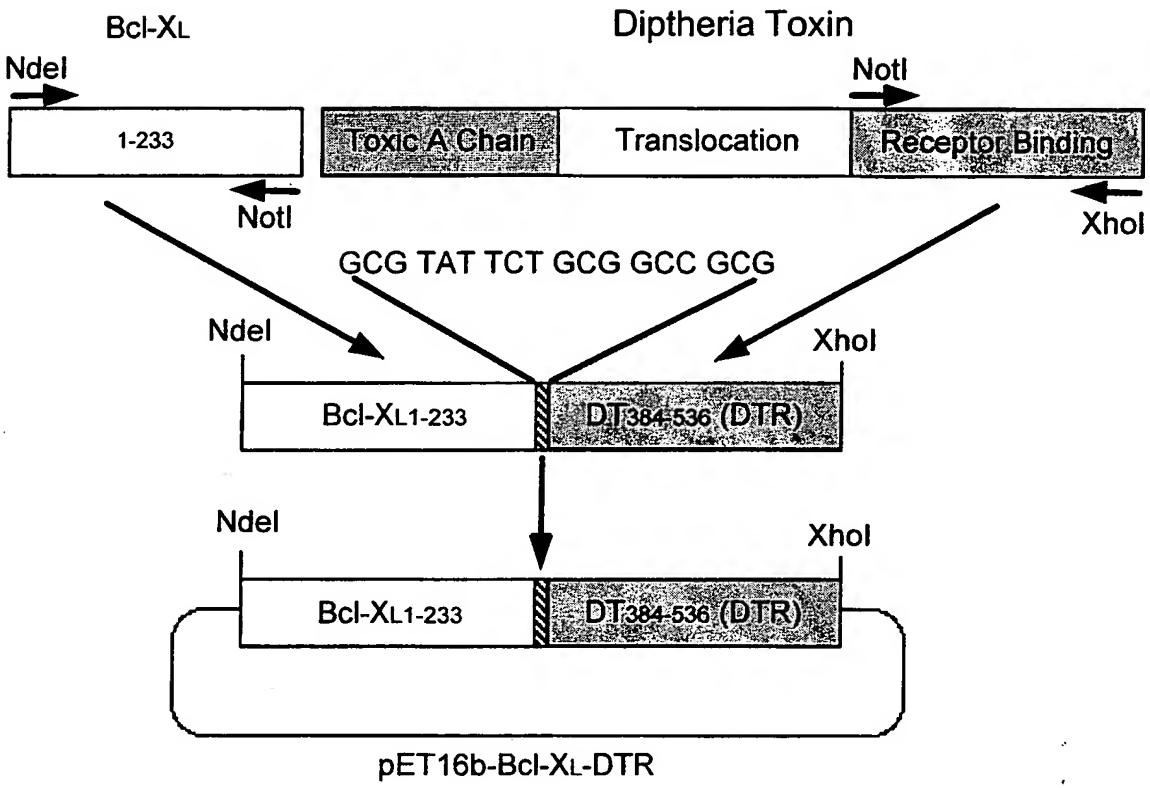

Bcl-XL
Diptheria Toxin
NdeI
NotI
1-233
Toxic A Chain
Translocation
Receptor Binding
NotI
XhoI
GCG TAT TCT GCG GCC GCG
NdeI
XhoI
Bcl-XL1-233
DT384-536 (DTR)
NdeI
XhoI
Bcl-XL1-233
DT384-536 (DTR)
pET16b-Bcl-XL-DTR

FIGURE 1A

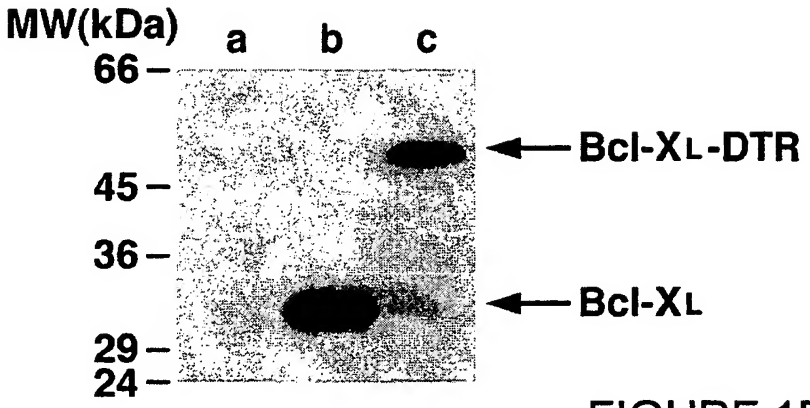


FIGURE 1B

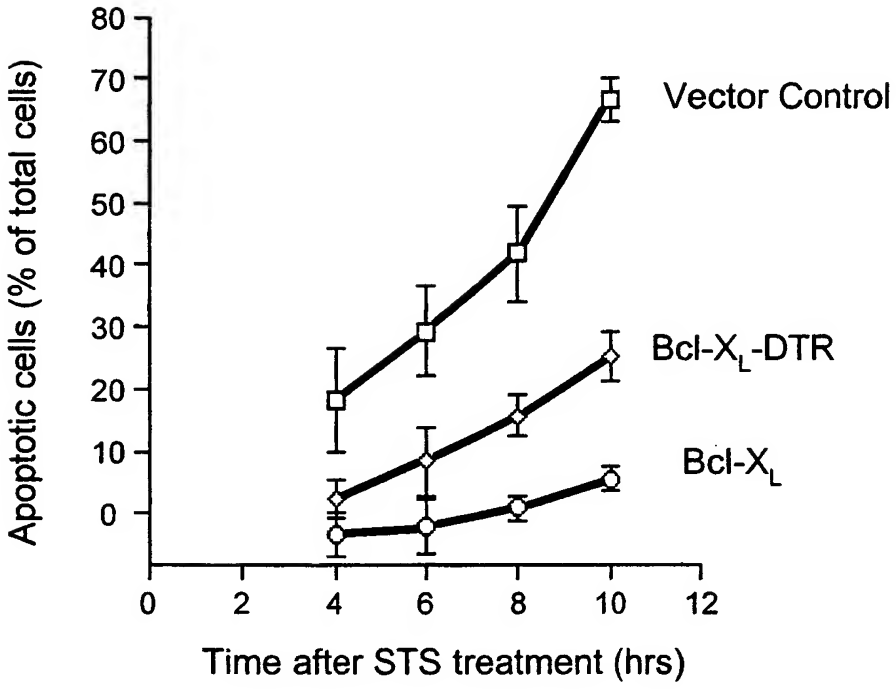


FIGURE 1C

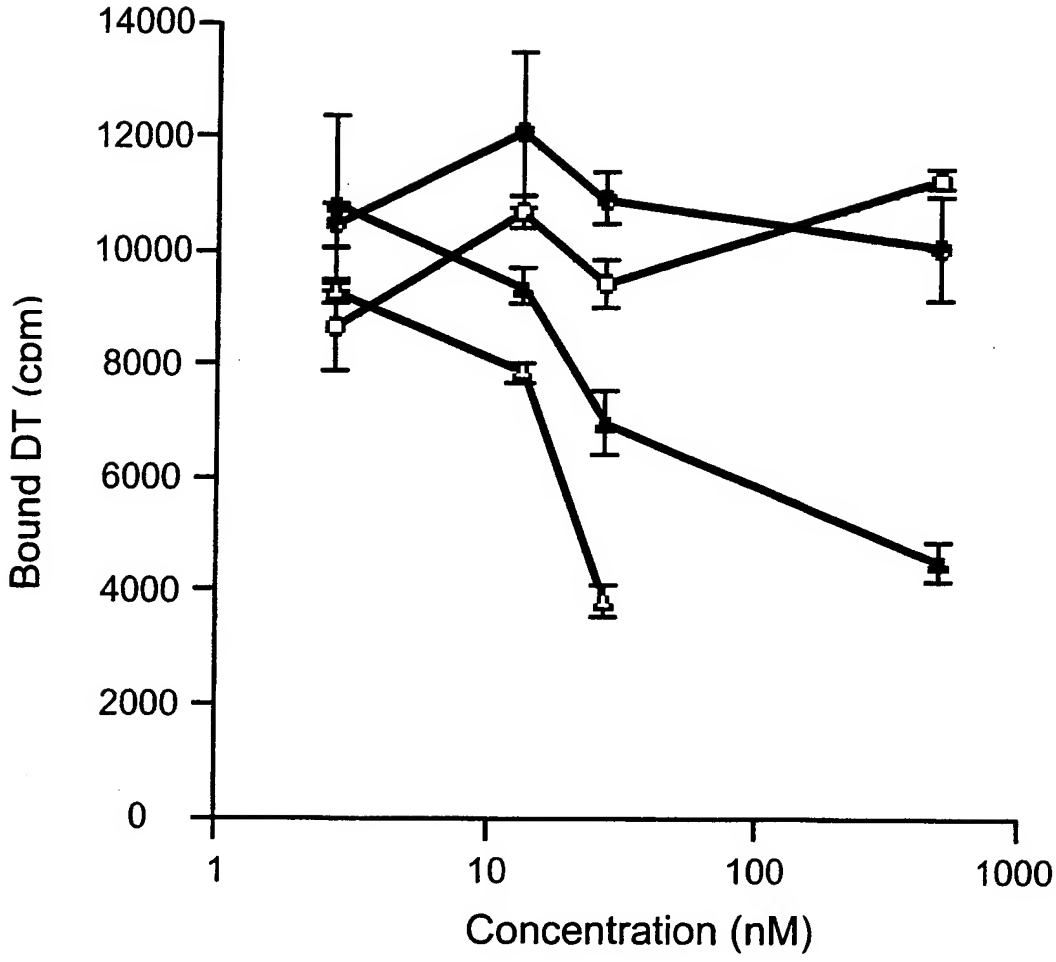

14000
12000
10000
8000
6000
4000
2000
0
Bound DT (cpm)
1
10
100
1000
Concentration (nM)

FIGURE 2

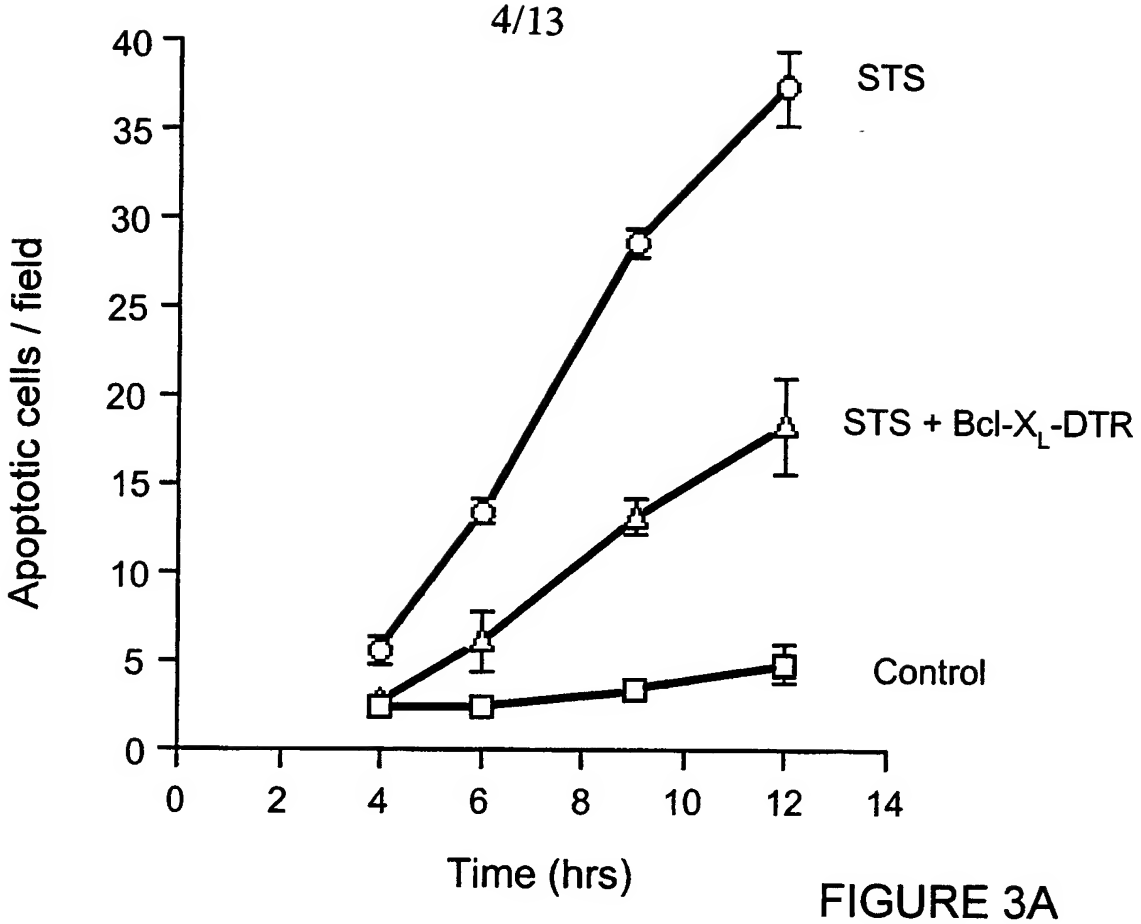


FIGURE 3A

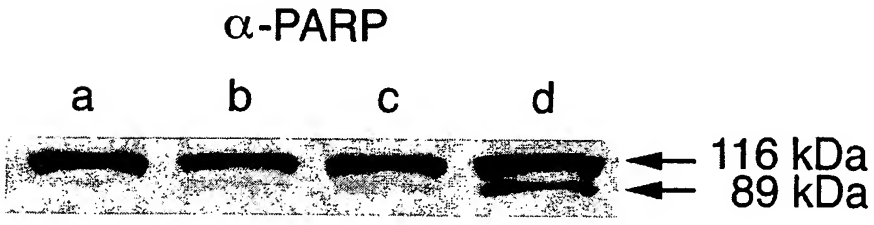


FIGURE 3B

FIGURE 4A

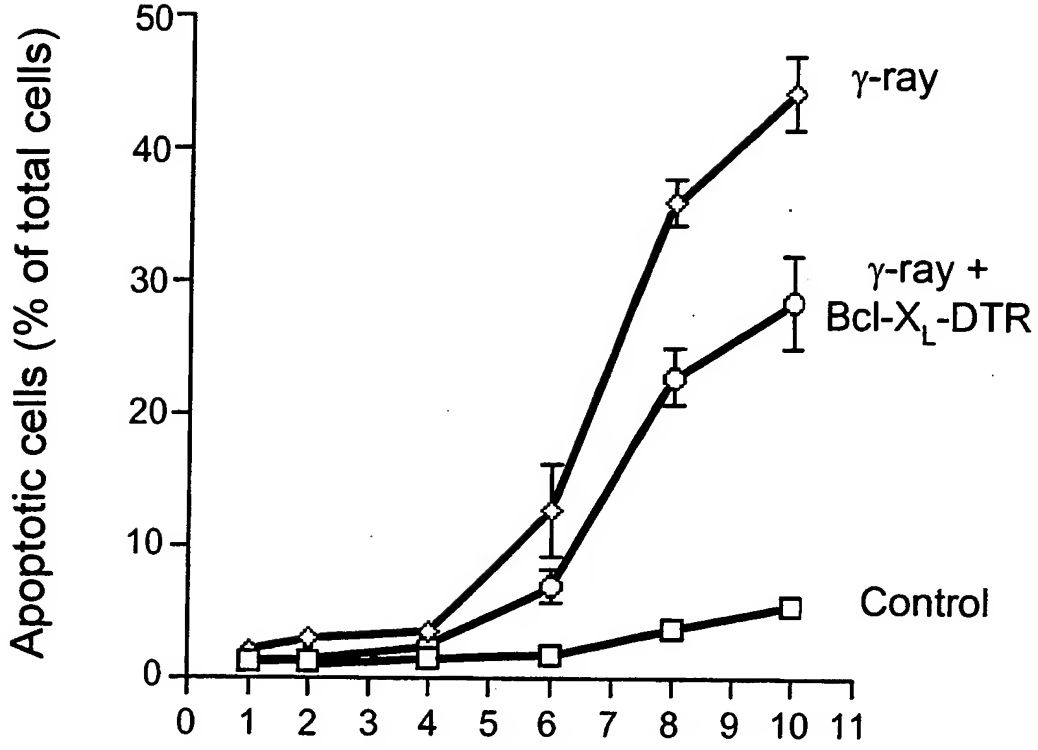
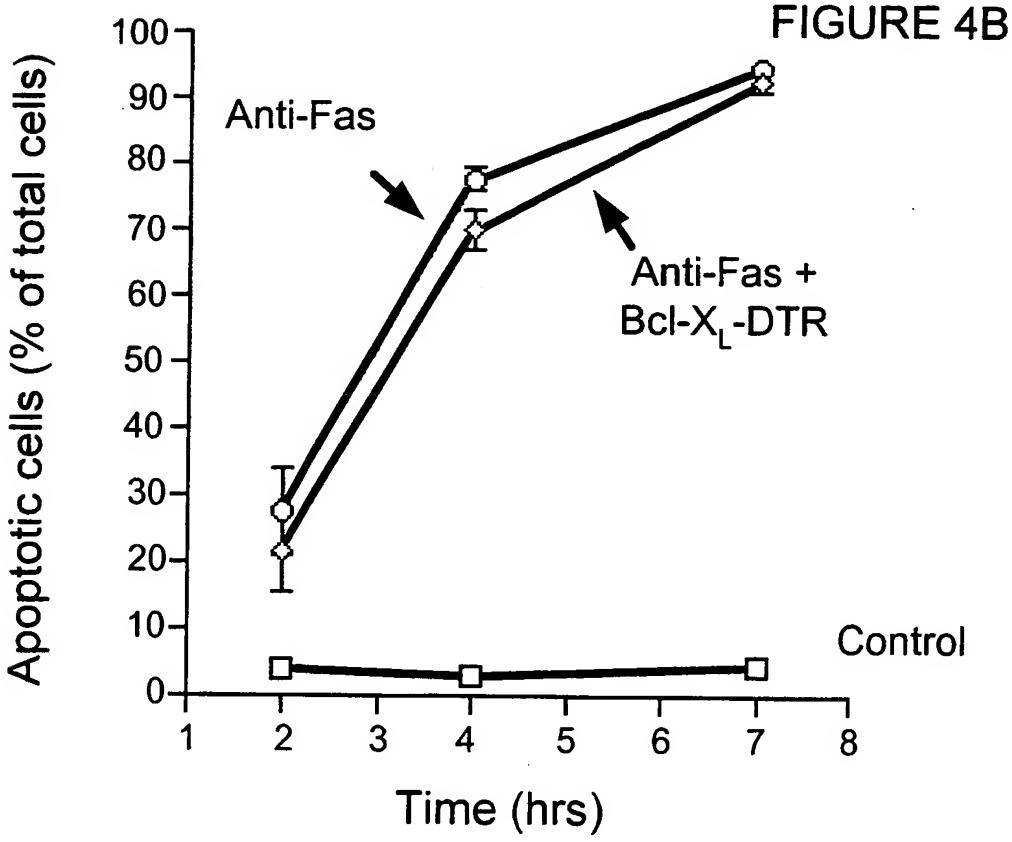


FIGURE 4B



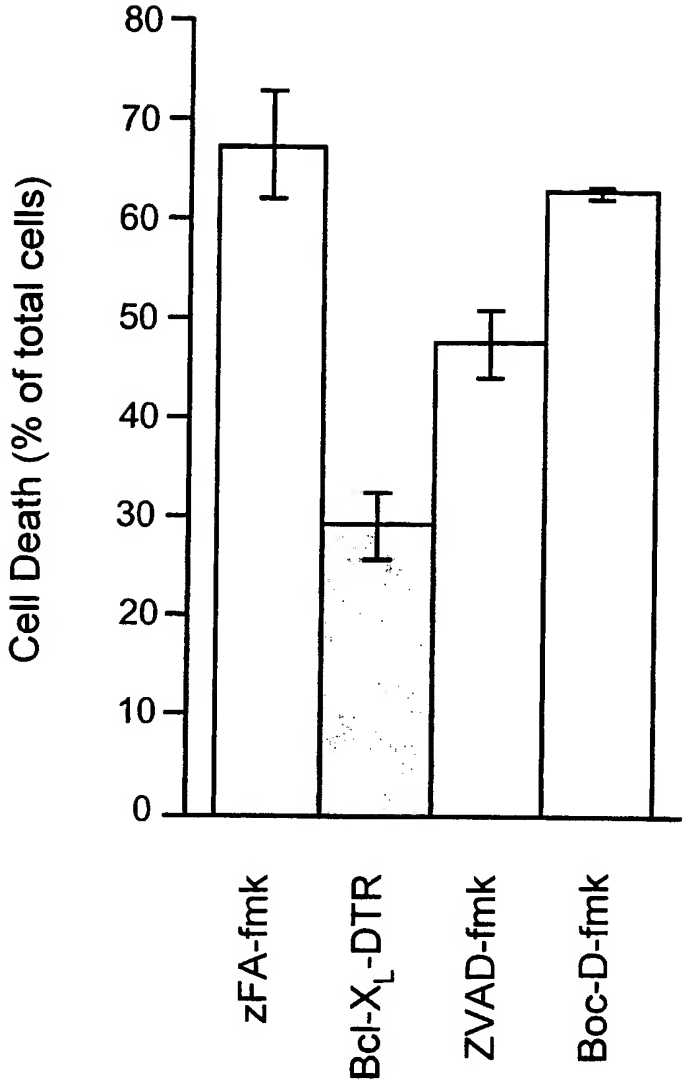

Cell Death (% of total cells)
80
70
60
50
40
30
20
10
0
zFA-fmk
Bcl-X$_L$-DTR
ZVAD-fmk
Boc-D-fmk

FIGURE 5

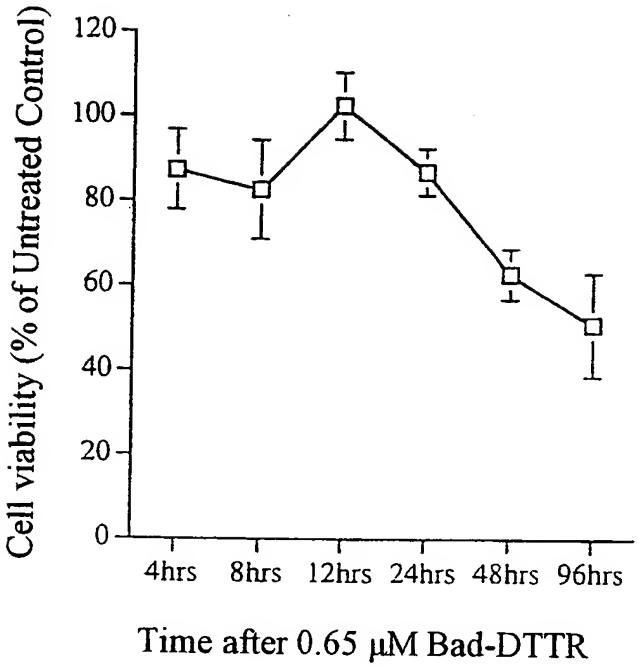

Cell viability (% of Untreated Control)
120
100
80
60
40
20
0
4hrs
8hrs
12hrs
24hrs
48hrs
96hrs
Time after 0.65 μM Bad-DTTR

FIGURE 6

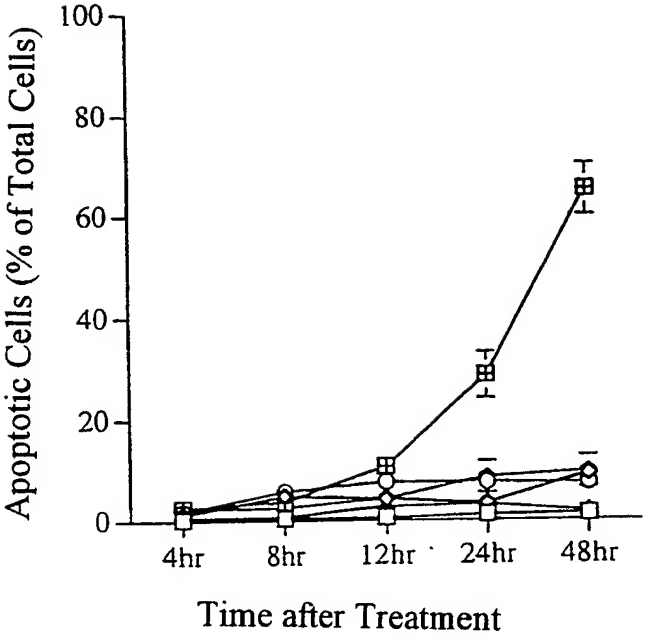


FIGURE 7A

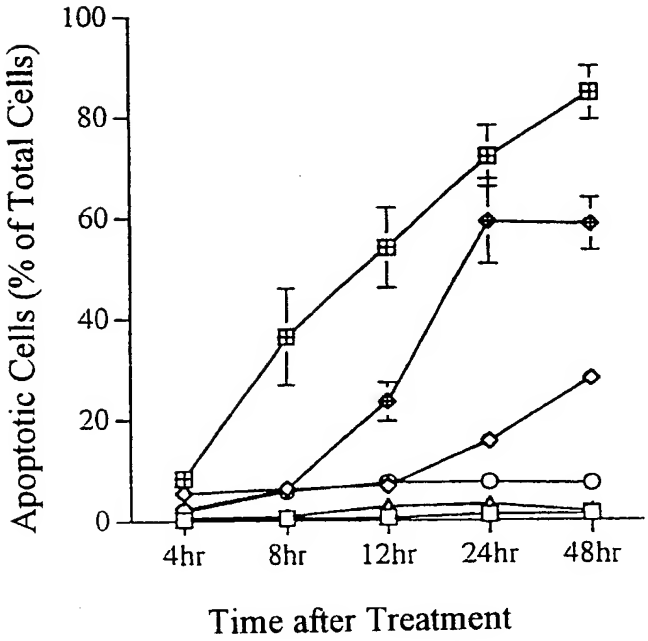


FIGURE 7B

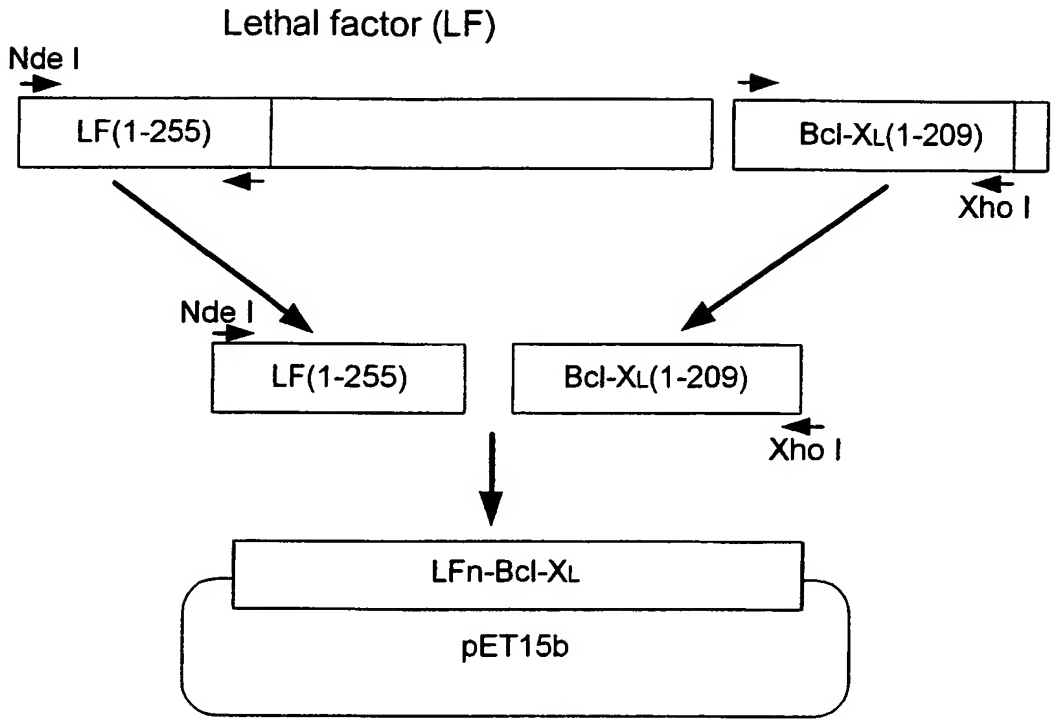

Lethal factor (LF)
Nde I
LF(1-255)
Bcl-XL(1-209)
Xho I
Nde I
LF(1-255)
Bcl-XL(1-209)
Xho I
LFn-Bcl-XL
pET15b

FIGURE 8

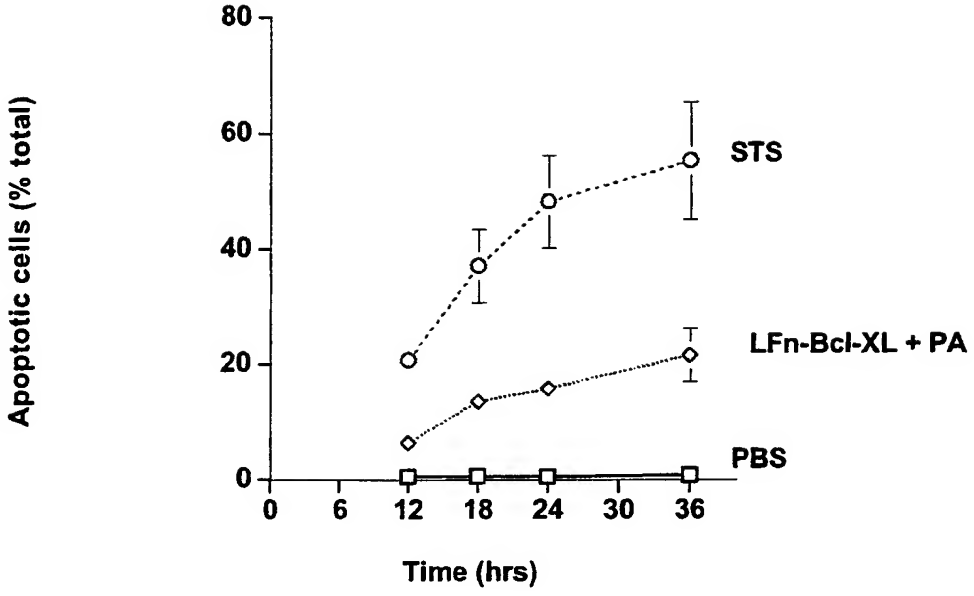

Apoptotic cells (% total)
80
60
40
20
0
0
6
12
18
24
30
36
Time (hrs)
STS
LFn-Bcl-XL + PA
PBS

FIGURE 9

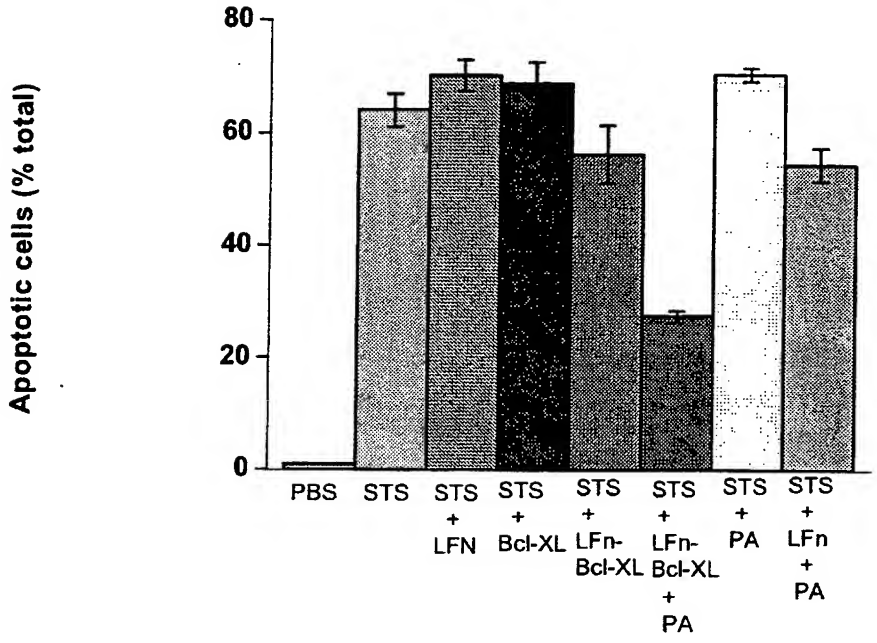

Apoptotic cells (% total)
80
60
40
20
0
PBS
STS
STS + LFN
STS + Bcl-XL
STS + LFn-Bcl-XL
STS + LFn-Bcl-XL + PA
STS + PA
STS + LFn + PA

FIGURE 10

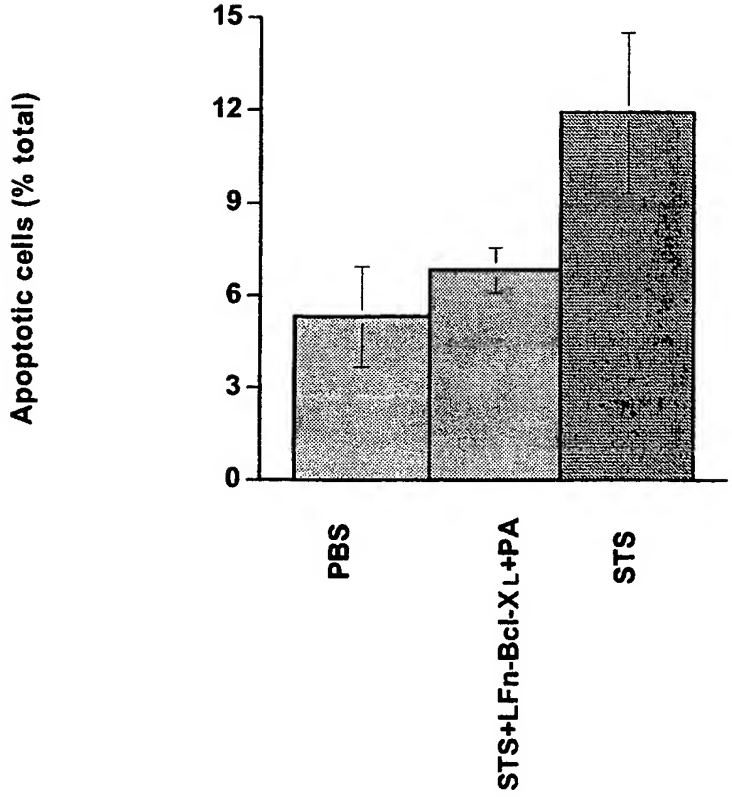


FIGURE 11

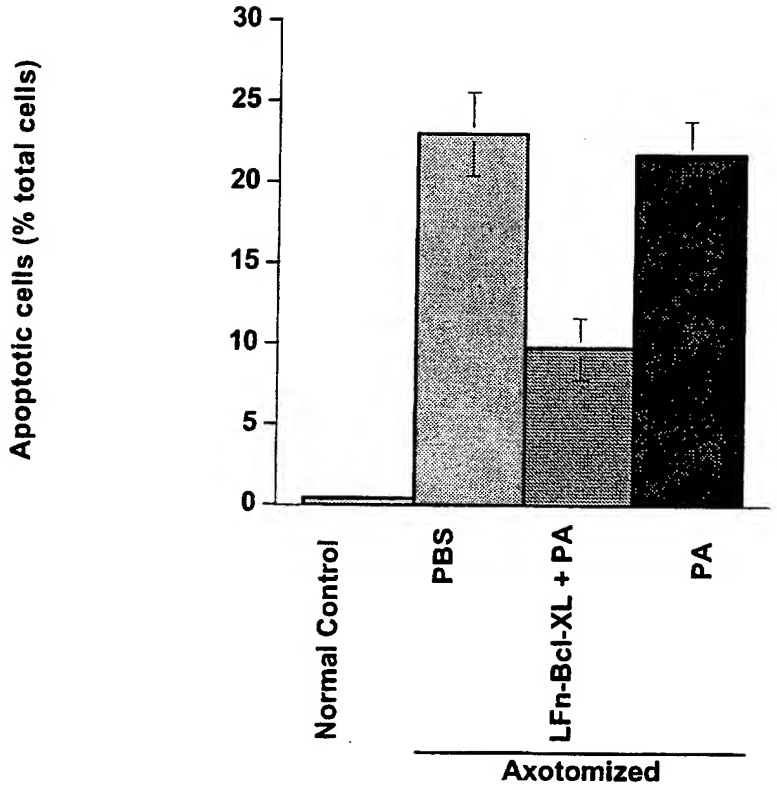

Apoptotic cells (% total cells)
30
25
20
15
10
5
0
Normal Control
PBS
LFn-Bcl-XL + PA
PA
Axotomized

FIGURE 12

SEQUENCE LISTING

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<120> RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-XL FUSION PROTEIN INHIBITS APOPTOSIS

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<170> PatentIn Ver. 2.1

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```
atg ggc cat cat cat cat cat cat cat cat cac agc agc ggc cat   48
Met Gly His His His His His His His His His Ser Ser Gly His
  1               5                  10                  15

atc gaa ggt cgt atg tct cag agc aac cgg gag ctg gtg gtt gac ttt   96
Ile Glu Gly Arg Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe
             20                  25                  30

ctc tcc tac aag ctt tcc cag aaa gga tac agc tgg agt cag ttt agt   144
Leu Ser Tyr Lys Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser
         35                  40                  45

gat gtg gaa gag aac agg act gag gcc cca gaa ggg act gaa tcg gag   192
Asp Val Glu Glu Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu
     50                  55                  60

atg gag acc ccc agt gcc atc aat ggc aac cca tcc tgg cac ctg gca   240
Met Glu Thr Pro Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala
 65                  70                  75                  80

gac agc ccc gcg gtg aat gga gcc act gcg cac agc agc agt ttg gat   288
Asp Ser Pro Ala Val Asn Gly Ala Thr Ala His Ser Ser Ser Leu Asp
                 85                  90                  95

gcc cgg gag gtg atc ccc atg gca gca gta aag caa gcg ctg agg gag   336
Ala Arg Glu Val Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu
            100                 105                 110

gca ggc gac gag ttt gaa ctg cgg tac cgg cgg gca ttc agt gac ctg   384
```

```
Ala Gly Asp Glu Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu
        115                 120                 125

aca tcc cag ctc cac atc acc cca ggg aca gca tat cag agc ttt gaa   432
Thr Ser Gln Leu His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu
    130                 135                 140

cag gta gtg aat gaa ctc ttc cgg gat ggg gta aac tgg ggt cgc att   480
Gln Val Val Asn Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile
145                 150                 155                 160

gtg gcc ttt ttc tcc ttc ggc ggg gca ctg tgc gtg gaa agc gta gac   528
Val Ala Phe Phe Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp
                165                 170                 175

aag gag atg cag gta ttg gtg agt cgg atc gca gct tgg atg gcc act   576
Lys Glu Met Gln Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr
            180                 185                 190

tac ctg aat gac cac cta gag cct tgg atc cag gag aac ggc ggc tgg   624
Tyr Leu Asn Asp His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp
        195                 200                 205

gat act ttt gtg gaa ctc tat ggg aac aat gca gca gcc gag agc cga   672
Asp Thr Phe Val Glu Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg
    210                 215                 220

aag ggc cag gaa cgc ttc aac cgc tgg ttc ctg acg ggc atg act gtg   720
Lys Gly Gln Glu Arg Phe Asn Arg Trp Phe Leu Thr Gly Met Thr Val
225                 230                 235                 240

gcc ggc gtg gtt ctg ctg ggc tca ctc ttc agt cgg aaa gcg tat tct   768
Ala Gly Val Val Leu Leu Gly Ser Leu Phe Ser Arg Lys Ala Tyr Ser
                245                 250                 255

gcg gcc gcg cat aaa acg caa cca ttt ctt cat gac ggg tat gct gtc   816
Ala Ala Ala His Lys Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val
            260                 265                 270

agt tgg aac act gtt gaa gat tcg ata atc cga act ggt ttt caa ggg   864
Ser Trp Asn Thr Val Glu Asp Ser Ile Ile Arg Thr Gly Phe Gln Gly
        275                 280                 285

gag agt ggg cac gac ata aaa att act gct gaa aat acc ccg ctt cca   912
Glu Ser Gly His Asp Ile Lys Ile Thr Ala Glu Asn Thr Pro Leu Pro
    290                 295                 300

atc gcg ggt gtc cta cta ccg act att cct gga aag ctg gac gtt aat   960
Ile Ala Gly Val Leu Leu Pro Thr Ile Pro Gly Lys Leu Asp Val Asn
305                 310                 315                 320

aag tcc aag act cat att tcc gta aat ggt cgg aaa ata agg atg cgt  1008
Lys Ser Lys Thr His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg
                325                 330                 335

tgc aga gct ata gac ggt gat gta act ttt tgt cgc cct aaa tct cct  1056
Cys Arg Ala Ile Asp Gly Asp Val Thr Phe Cys Arg Pro Lys Ser Pro
            340                 345                 350

gtt tat gtt ggt aat ggt gtg cat gcg aat ctt cac gtg gca ttt cac  1104
Val Tyr Val Gly Asn Gly Val His Ala Asn Leu His Val Ala Phe His
```

```
        355                 360                 365

aga agc agc tcg gag aaa att cat tct aat gaa att tcg tcg gat tcc   1152
Arg Ser Ser Ser Glu Lys Ile His Ser Asn Glu Ile Ser Ser Asp Ser
    370                 375                 380

ata ggc gtt ctt ggg tac cag aaa aca gta gat cac acc aag gtt aat   1200
Ile Gly Val Leu Gly Tyr Gln Lys Thr Val Asp His Thr Lys Val Asn
385                 390                 395                 400

tct aag cta tcg cta ttt ttt gaa atc aaa agc tga                   1236
Ser Lys Leu Ser Leu Phe Phe Glu Ile Lys Ser
                405                 410
```

<210> 2
<211> 411
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: genetic fusion

<400> 2

```
Met Gly His His His His His His His His His His Ser Ser Gly His
  1               5                  10                  15
Ile Glu Gly Arg Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe
            20                  25                  30
Leu Ser Tyr Lys Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser
        35                  40                  45
Asp Val Glu Glu Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu
    50                  55                  60
Met Glu Thr Pro Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala
65                  70                  75                  80
Asp Ser Pro Ala Val Asn Gly Ala Thr Ala His Ser Ser Ser Leu Asp
                85                  90                  95
Ala Arg Glu Val Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu
            100                 105                 110
Ala Gly Asp Glu Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu
        115                 120                 125
Thr Ser Gln Leu His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu
    130                 135                 140
Gln Val Val Asn Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile
145                 150                 155                 160
Val Ala Phe Phe Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp
                165                 170                 175
Lys Glu Met Gln Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr
            180                 185                 190
Tyr Leu Asn Asp His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp
        195                 200                 205
Asp Thr Phe Val Glu Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg
    210                 215                 220
Lys Gly Gln Glu Arg Phe Asn Arg Trp Phe Leu Thr Gly Met Thr Val
225                 230                 235                 240
Ala Gly Val Val Leu Leu Gly Ser Leu Phe Ser Arg Lys Ala Tyr Ser
                245                 250                 255
Ala Ala Ala His Lys Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val
            260                 265                 270
Ser Trp Asn Thr Val Glu Asp Ser Ile Ile Arg Thr Gly Phe Gln Gly
        275                 280                 285
Glu Ser Gly His Asp Ile Lys Ile Thr Ala Glu Asn Thr Pro Leu Pro
    290                 295                 300
Ile Ala Gly Val Leu Leu Pro Thr Ile Pro Gly Lys Leu Asp Val Asn
```

```
305                 310                 315                 320
Lys Ser Lys Thr His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg
                325                 330                 335
Cys Arg Ala Ile Asp Gly Asp Val Thr Phe Cys Arg Pro Lys Ser Pro
            340                 345                 350
Val Tyr Val Gly Asn Gly Val His Ala Asn Leu His Val Ala Phe His
        355                 360                 365
Arg Ser Ser Ser Glu Lys Ile His Ser Asn Glu Ile Ser Ser Asp Ser
    370                 375                 380
Ile Gly Val Leu Gly Tyr Gln Lys Thr Val Asp His Thr Lys Val Asn
385                 390                 395                 400
Ser Lys Leu Ser Leu Phe Phe Glu Ile Lys Ser
                405                 410
```

<210> 3
<211> 1704
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: genetic fusion

<220>
<221> CDS
<222> (1)..(1704)

<400> 3

```
atg ggc cat cat cat cat cat cat cat cat cat cac agc agc ggc cat   48
Met Gly His His His His His His His His His His Ser Ser Gly His
  1               5                  10                  15

atc gaa ggt cgt cat atg gga acc cca aag cag ccc tcg ctg gct cct   96
Ile Glu Gly Arg His Met Gly Thr Pro Lys Gln Pro Ser Leu Ala Pro
             20                  25                  30

gca cac gcc cta ggc ttg agg aag tcc gat ccc gga atc cgg agc ctg   144
Ala His Ala Leu Gly Leu Arg Lys Ser Asp Pro Gly Ile Arg Ser Leu
         35                  40                  45

ggg agc gac gcg gga gga agg cgg tgg aga cca gca gcc cag agt atg   192
Gly Ser Asp Ala Gly Gly Arg Arg Trp Arg Pro Ala Ala Gln Ser Met
     50                  55                  60

ttc cag atc cca gag ttt gag ccg agt gag cag gaa gac gct agt gct   240
Phe Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ala Ser Ala
 65                  70                  75                  80

aca gat agg ggc ctg ggc cct agc ctc act gag gac cag cca ggt ccc   288
Thr Asp Arg Gly Leu Gly Pro Ser Leu Thr Glu Asp Gln Pro Gly Pro
                 85                  90                  95

tac ctg gcc cca ggt ctc ctg ggg agc aac att cat cag cag gga cgg   336
Tyr Leu Ala Pro Gly Leu Leu Gly Ser Asn Ile His Gln Gln Gly Arg
            100                 105                 110

gca gcc acc aac agt cat cat gga ggc gca ggg gct atg gag act cgg   384
Ala Ala Thr Asn Ser His His Gly Gly Ala Gly Ala Met Glu Thr Arg
        115                 120                 125
```

```
agt cgc cac agt gcg tac cca gcg ggg acc gag gag gat gaa ggg atg   432
Ser Arg His Ser Ala Tyr Pro Ala Gly Thr Glu Glu Asp Glu Gly Met
    130                 135                 140

gag gag gag ctt agc cct ttt cga gga cgc tcg cgt gcg gct ccc ccc   480
Glu Glu Glu Leu Ser Pro Phe Arg Gly Arg Ser Arg Ala Ala Pro Pro
145                 150                 155                 160

aat ctc tgg gca gcg cag cgc tac ggc cgt gag ctc cga agg atg agc   528
Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
                165                 170                 175

gat gag ttt gag ggt tcc ttc aag gga ctt cct cgc cca aag agc gca   576
Asp Glu Phe Glu Gly Ser Phe Lys Gly Leu Pro Arg Pro Lys Ser Ala
            180                 185                 190

ggc act gca aca cag atg cga caa agc gcc ggc tgg acg cgc att atc   624
Gly Thr Ala Thr Gln Met Arg Gln Ser Ala Gly Trp Thr Arg Ile Ile
        195                 200                 205

cag tcc tgg tgg gat cga aac ttg ggc aaa gga ggc tcc acc ccc tcc   672
Gln Ser Trp Trp Asp Arg Asn Leu Gly Lys Gly Gly Ser Thr Pro Ser
    210                 215                 220

cag tca gta ggt agc tca ttg tca tgc ata aat ctt gat tgg gat gtc   720
Gln Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val
225                 230                 235                 240

ata agg gat aaa act aag aca aag ata gag tct ttg aaa gag cat ggc   768
Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly
                245                 250                 255

cct atc aaa aat aaa atg agc gaa agt ccc aat aaa aca gta tct gag   816
Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu
            260                 265                 270

gaa aaa gct aaa caa tac cta gaa gaa ttt cat caa acg gca tta gag   864
Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu Glu
        275                 280                 285

cat cct gaa ttg tca gaa ctt aaa acc gtt act ggg acc aat cct gta   912
His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro Val
    290                 295                 300

ttc gct ggg gct aac tat gcg gcg tgg gca gta aac gtt gcg caa gtt   960
Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val
305                 310                 315                 320

atc gat agc gaa aca gct gat aat ttg gaa aag aca act gct gct ctt  1008
Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu
                325                 330                 335

tcg ata ctt cct ggt atc ggt agc gta atg ggc att gca gac ggt gcc  1056
Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala
            340                 345                 350

gtt cac cac aat aca gaa gag ata gtg gca caa tca ata gct tta tcg  1104
Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser
        355                 360                 365

tct tta atg gtt gct caa gct att cca ttg gta gga gag cta gtt gat  1152
```

```
Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp
    370                 375                 380

att ggt ttc gct gca tat aat ttt gta gag agt att atc aat tta ttt   1200
Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu Phe
385                 390                 395                 400

caa gta gtt cat aat tcg tat aat cgt ccc gcg tat tct ccg ggg cat   1248
Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly His
                405                 410                 415

aaa acg caa cca ttt ctt cat gac ggg tat gct gtc agt tgg aac act   1296
Lys Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val Ser Trp Asn Thr
            420                 425                 430

gtt gaa gat tcg ata atc cga act ggt ttt caa ggg gag agt ggg cac   1344
Val Glu Asp Ser Ile Ile Arg Thr Gly Phe Gln Gly Glu Ser Gly His
        435                 440                 445

gac ata aaa att act gct gaa aat acc ccg ctt cca atc gcg ggt gtc   1392
Asp Ile Lys Ile Thr Ala Glu Asn Thr Pro Leu Pro Ile Ala Gly Val
    450                 455                 460

cta cta ccg act att cct gga aag ctg gac gtt aat aag tcc aag act   1440
Leu Leu Pro Thr Ile Pro Gly Lys Leu Asp Val Asn Lys Ser Lys Thr
465                 470                 475                 480

cat att tcc gta aat ggt cgg aaa ata agg atg cgt tgc aga gct ata   1488
His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg Cys Arg Ala Ile
                485                 490                 495

gac ggt gat gta act ttt tgt cgc cct aaa tct cct gtt tat gtt ggt   1536
Asp Gly Asp Val Thr Phe Cys Arg Pro Lys Ser Pro Val Tyr Val Gly
            500                 505                 510

aat ggt gtg cat gcg aat ctt cac gtg gca ttt cac aga agc agc tcg   1584
Asn Gly Val His Ala Asn Leu His Val Ala Phe His Arg Ser Ser Ser
        515                 520                 525

gag aaa att cat tct aat gaa att tcg tcg gat tcc ata ggc gtt ctt   1632
Glu Lys Ile His Ser Asn Glu Ile Ser Ser Asp Ser Ile Gly Val Leu
    530                 535                 540

ggg tac cag aaa aca gta gat cac acc aag gtt aat tct aag cta tcg   1680
Gly Tyr Gln Lys Thr Val Asp His Thr Lys Val Asn Ser Lys Leu Ser
545                 550                 555                 560

cta ttt ttt gaa atc aaa agc tga                                  1704
Leu Phe Phe Glu Ile Lys Ser
                565
```

<210> 4
<211> 567
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: genetic fusion

<400> 4

```
Met Gly His His His His His His His His His His Ser Ser Gly His
  1               5                  10                  15
```

```
Ile Glu Gly Arg His Met Gly Thr Pro Lys Gln Pro Ser Leu Ala Pro
            20                  25                  30
Ala His Ala Leu Gly Leu Arg Lys Ser Asp Pro Gly Ile Arg Ser Leu
        35                  40                  45
Gly Ser Asp Ala Gly Gly Arg Arg Trp Arg Pro Ala Ala Gln Ser Met
    50                  55                  60
Phe Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ala Ser Ala
65                  70                  75                  80
Thr Asp Arg Gly Leu Gly Pro Ser Leu Thr Glu Asp Gln Pro Gly Pro
                85                  90                  95
Tyr Leu Ala Pro Gly Leu Leu Gly Ser Asn Ile His Gln Gln Gly Arg
            100                 105                 110
Ala Ala Thr Asn Ser His His Gly Gly Ala Gly Ala Met Glu Thr Arg
        115                 120                 125
Ser Arg His Ser Ala Tyr Pro Ala Gly Thr Glu Glu Asp Glu Gly Met
    130                 135                 140
Glu Glu Glu Leu Ser Pro Phe Arg Gly Arg Ser Arg Ala Ala Pro Pro
145                 150                 155                 160
Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
                165                 170                 175
Asp Glu Phe Glu Gly Ser Phe Lys Gly Leu Pro Arg Pro Lys Ser Ala
            180                 185                 190
Gly Thr Ala Thr Gln Met Arg Gln Ser Ala Gly Trp Thr Arg Ile Ile
        195                 200                 205
Gln Ser Trp Trp Asp Arg Asn Leu Gly Lys Gly Gly Ser Thr Pro Ser
    210                 215                 220
Gln Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val
225                 230                 235                 240
Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly
                245                 250                 255
Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val Ser Glu
            260                 265                 270
Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu Glu
        275                 280                 285
His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro Val
    290                 295                 300
Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln Val
305                 310                 315                 320
Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu
                325                 330                 335
Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala
            340                 345                 350
Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser
        355                 360                 365
Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp
    370                 375                 380
Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu Phe
385                 390                 395                 400
Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly His
                405                 410                 415
Lys Thr Gln Pro Phe Leu His Asp Gly Tyr Ala Val Ser Trp Asn Thr
            420                 425                 430
Val Glu Asp Ser Ile Ile Arg Thr Gly Phe Gln Gly Glu Ser Gly His
        435                 440                 445
Asp Ile Lys Ile Thr Ala Glu Asn Thr Pro Leu Pro Ile Ala Gly Val
    450                 455                 460
Leu Leu Pro Thr Ile Pro Gly Lys Leu Asp Val Asn Lys Ser Lys Thr
465                 470                 475                 480
His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg Cys Arg Ala Ile
                485                 490                 495
Asp Gly Asp Val Thr Phe Cys Arg Pro Lys Ser Pro Val Tyr Val Gly
```

```
            500                 505                 510
Asn Gly Val His Ala Asn Leu His Val Ala Phe His Arg Ser Ser Ser
        515                 520                 525
Glu Lys Ile His Ser Asn Glu Ile Ser Ser Asp Ser Ile Gly Val Leu
    530                 535                 540
Gly Tyr Gln Lys Thr Val Asp His Thr Lys Val Asn Ser Lys Leu Ser
545                 550                 555                 560
Leu Phe Phe Glu Ile Lys Ser
                565
```

<210> 5
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide linker

<400> 5
gcgtattctg cggccgcg 18

<210> 6
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligopeptide
linker

<400> 6
Ala Tyr Ser Ala Ala Ala
1 5

<210> 7
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: genetic fusion

<220>
<221> CDS
<222> (1)..(1455)

<400> 7
atg ggc agc agc cat cat cat cat cat cac agc agc ggc ctg gtg ccg 48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15

cgc ggc agc cat atg gcg ggc ggt cat ggt gat gta ggt atg cac gta 96
Arg Gly Ser His Met Ala Gly Gly His Gly Asp Val Gly Met His Val
20 25 30

aaa gag aaa gag aaa aat aaa gat gag aat aag aga aaa gat gaa gaa 144

```
Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp Glu Glu
          35                  40                  45

cga aat aaa aca cag gaa gag cat tta aag gaa atc atg aaa cac att   192
Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu Ile Met Lys His Ile
     50                  55                  60

gta aaa ata gaa gta aaa ggg gag gaa gct gtt aaa aaa gag gca gca   240
Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val Lys Lys Glu Ala Ala
 65                  70                  75                  80

gaa aag cta ctt gag aaa gta cca tct gat gtt tta gag atg tat aaa   288
Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val Leu Glu Met Tyr Lys
                 85                  90                  95

gca att gga gga aag ata tat att gtg gat ggt gat att aca aaa cat   336
Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr Lys His
            100                 105                 110

ata tct tta gaa gca tta tct gaa gat aag aaa aaa ata aaa gac att   384
Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys Asp Ile
        115                 120                 125

tat ggg aaa gat gct tta tta cat gaa cat tat gta tat gca aaa gaa   432
Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr Val Tyr Ala Lys Glu
    130                 135                 140

gga tat gaa ccc gta ctt gta atc caa tct tcg gaa gat tat gta gaa   480
Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser Glu Asp Tyr Val Glu
145                 150                 155                 160

aat act gaa aag gca ctg aac gtt tat tat gaa ata ggt aag ata tta   528
Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys Ile Leu
                165                 170                 175

tca agg gat att tta agt aaa att aat caa cca tat cag aaa ttt tta   576
Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys Phe Leu
            180                 185                 190

gat gta tta aat acc att aaa aat gca tct gat tca gat gga caa gat   624
Asp Val Leu Asn Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly Gln Asp
        195                 200                 205

ctt tta ttt act aat cag ctt aag gaa cat ccc aca gac ttt tct gta   672
Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro Thr Asp Phe Ser Val
    210                 215                 220

gaa ttc ttg gaa caa aat agc aat gag gta caa gaa gta ttt gcg aaa   720
Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln Glu Val Phe Ala Lys
225                 230                 235                 240

gct ttt gca tat tat atc gag cca cag cat cgt gat gtt tta cag ctt   768
Ala Phe Ala Tyr Tyr Ile Glu Pro Gln His Arg Asp Val Leu Gln Leu
                245                 250                 255

tat gca ccg gaa gct ttt aat tac atg gat aaa ttt aac gaa caa gaa   816
Tyr Ala Pro Glu Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu Gln Glu
            260                 265                 270

ata aat cta tcc atg tct cag agc aac cgg gag ctg gtg gtt gac ttt   864
Ile Asn Leu Ser Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe
```

```
        275                 280                 285

ctc tcc tac aag ctt tcc cag aaa gga tac agc tgg agt cag ttt agt   912
Leu Ser Tyr Lys Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser
    290                 295                 300

gat gtg gaa gag aac agg act gag gcc cca gaa ggg act gaa tcg gag   960
Asp Val Glu Glu Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu
305                 310                 315                 320

atg gag acc ccc agt gcc atc aat ggc aac cca tcc tgg cac ctg gca  1008
Met Glu Thr Pro Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala
                325                 330                 335

gac agc ccc gcg gtg aat gga gcc act gcg cac agc agc agt ttg gat  1056
Asp Ser Pro Ala Val Asn Gly Ala Thr Ala His Ser Ser Ser Leu Asp
            340                 345                 350

gcc cgg gag gtg atc ccc atg gca gca gta aag caa gcg ctg agg gag  1104
Ala Arg Glu Val Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu
        355                 360                 365

gca ggc gac gag ttt gaa ctg cgg tac cgg cgg gca ttc agt gac ctg  1152
Ala Gly Asp Glu Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu
    370                 375                 380

aca tcc cag ctc cac atc acc cca ggg aca gca tat cag agc ttt gaa  1200
Thr Ser Gln Leu His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu
385                 390                 395                 400

cag gta gtg aat gaa ctc ttc cgg gat ggg gta aac tgg ggt cgc att  1248
Gln Val Val Asn Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile
                405                 410                 415

gtg gcc ttt ttc tcc ttc ggc ggg gca ctg tgc gtg gaa agc gta gac  1296
Val Ala Phe Phe Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp
            420                 425                 430

aag gag atg cag gta ttg gtg agt cgg atc gca gct tgg atg gcc act  1344
Lys Glu Met Gln Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr
        435                 440                 445

tac ctg aat gac cac cta gag cct tgg atc cag gag aac ggc ggc tgg  1392
Tyr Leu Asn Asp His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp
    450                 455                 460

gat act ttt gtg gaa ctc tat ggg aac aat gca gca gcc gag agc cga  1440
Asp Thr Phe Val Glu Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg
465                 470                 475                 480

aag ggc cag gaa cgc                                             1455
Lys Gly Gln Glu Arg
                485
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<210> 8
<211> 485
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: genetic fusion

<400> 8

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Arg Gly Ser His Met Ala Gly Gly His Gly Asp Val Gly Met His Val
             20                  25                  30

Lys Glu Lys Glu Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp Glu Glu
         35                  40                  45

Arg Asn Lys Thr Gln Glu Glu His Leu Lys Glu Ile Met Lys His Ile
     50                  55                  60

Val Lys Ile Glu Val Lys Gly Glu Glu Ala Val Lys Lys Glu Ala Ala
 65                  70                  75                  80

Glu Lys Leu Leu Glu Lys Val Pro Ser Asp Val Leu Glu Met Tyr Lys
                 85                  90                  95

Ala Ile Gly Gly Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr Lys His
            100                 105                 110

Ile Ser Leu Glu Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys Asp Ile
        115                 120                 125

Tyr Gly Lys Asp Ala Leu Leu His Glu His Tyr Val Tyr Ala Lys Glu
    130                 135                 140

Gly Tyr Glu Pro Val Leu Val Ile Gln Ser Ser Glu Asp Tyr Val Glu
145                 150                 155                 160

Asn Thr Glu Lys Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys Ile Leu
                165                 170                 175

Ser Arg Asp Ile Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys Phe Leu
            180                 185                 190

Asp Val Leu Asn Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly Gln Asp
        195                 200                 205

Leu Leu Phe Thr Asn Gln Leu Lys Glu His Pro Thr Asp Phe Ser Val
    210                 215                 220

Glu Phe Leu Glu Gln Asn Ser Asn Glu Val Gln Glu Val Phe Ala Lys
225                 230                 235                 240

Ala Phe Ala Tyr Tyr Ile Glu Pro Gln His Arg Asp Val Leu Gln Leu
                245                 250                 255

Tyr Ala Pro Glu Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu Gln Glu
            260                 265                 270

Ile Asn Leu Ser Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe
        275                 280                 285

Leu Ser Tyr Lys Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser
    290                 295                 300

Asp Val Glu Glu Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu
305                 310                 315                 320
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Met Glu Thr Pro Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala
325 330 335

Asp Ser Pro Ala Val Asn Gly Ala Thr Ala His Ser Ser Ser Leu Asp
340 345 350

Ala Arg Glu Val Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu
355 360 365

Ala Gly Asp Glu Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu
370 375 380

Thr Ser Gln Leu His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu
385 390 395 400

Gln Val Val Asn Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile
405 410 415

Val Ala Phe Phe Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp
420 425 430

Lys Glu Met Gln Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr
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Tyr Leu Asn Asp His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp
450 455 460

Asp Thr Phe Val Glu Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg
465 470 475 480

Lys Gly Gln Glu Arg
485

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(54) Title: RECEPTOR-MEDIATED UPTAKE OF AN EXTRACELLULAR BCL-x_L FUSION PROTEIN INHIBITS APOPTOSIS

(57) Abstract: Apoptosis-modifying fusion polypeptides, and the corresponding nucleic acid molecules, are disclosed. Pharmaceutical compositions comprising these polypeptides, and the use of these polypeptides to modify apoptosis are also provided.

INTERNATIONAL SEARCH REPORT

Int[illegible]ional Application No
PCT/US 00/22293

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C07K14/47 C07K14/34 C07K19/00 C12N15/62 C12N15/63
C12N5/10 A61K38/16

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C07K C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal, WPI Data, PAJ, BIOSIS, STRAND

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 17682 A (WASHINGTON UNIVERSITY) 30 April 1998 (1998-04-30) SEQ ID NO:14, SEQ ID NO:16 page 24, line 9-26; claim 13 --- -/--	1,2,11, 12, 16-18, 20,26, 46,47, 49,50, 53,60,61

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
7 February 2001	22/02/2001

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Schönwasser, D

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INTERNATIONAL SEARCH REPORT

Inte ional Application No
PCT/US 00/22293

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

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P,X	LIU X.-H. ET AL.: "Receptor-mediated uptake of an extracellular Bcl-x(l) fusion protein inhibits apoptosis" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES, USA, vol. 96, no. 17, 17 August 1999 (1999-08-17), pages 9563-9567, XP002159673 the whole document	1-15, 20-22, 24-32, 34-37, 42-46, 49, 52-55, 60,61
P,X	WO 99 45128 A (YISSUM RES DEV CO) 10 September 1999 (1999-09-10) page 9, line 1 -page 10, line 5 page 13, line 26 -page 17, line 24	1,2, 10-12, 21,23, 26,27, 46,47, 49,50, 53,60,61
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A	BOISE L H ET AL: "BCL-X, A BCL-2-RELATED GENE THAT FUNCTIONS AS A DOMINANT REGULATOR OF APOPTOTIC CELL DEATH" CELL, vol. 74, 27 August 1993 (1993-08-27), pages 597-608, XP002018919 ISSN: 0092-8674 figures 1,3	4-9
A	WO 94 18332 A (US HEALTH) 18 August 1994 (1994-08-18) SEQ ID NO:1, SEQ ID NO:2	4-9
A	NEWTON K. ET AL.: "The Bcl-2 family and cell death regulation" CURRENT OPINION IN GENETICS & DEVELOPMENT, vol. 8, no. 1, February 1998 (1998-02), pages 68-75, XP000926158 the whole document	1-61

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